

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 25, 2001, 16:50:26 ; Search time 22.51 Seconds
(without alignments)
16.920 Million cell updates/sec

Title: US-09-251-638-2
Perfect score: 27
Sequence: 1 GvGVP 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR:68:
1: pir1:
2: pir2:
3: pir3:
4: pir4:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	27	100.0	38	2 T46593	phytoene dehydrogenase [imported] - Mycobacterium marinum (fragment)
2	27	100.0	84	2 S03384	phytoene dehydrogenase hypothetical prote
3	27	100.0	97	2 C96743	unknown protein [I]
4	27	100.0	161	2 S33491	hypothetical prote
5	27	100.0	206	2 T10113	hypothetical prote
6	27	100.0	208	2 D64301	hypothetical prote
7	27	100.0	211	2 S73791	hypothetical prote
8	27	100.0	214	2 T23593	hypothetical prote
9	27	100.0	256	2 G39845	dihydroorotate dehydrogenase
10	27	100.0	277	2 S78063	homeobox protein P
11	27	100.0	281	2 JC4558	viomycin kinase (E)
12	27	100.0	290	2 S67297	hypothetical prote
13	27	100.0	303	2 F0693	probable UPPA protein
14	27	100.0	308	2 BT5292	glucokinase - Dein
15	27	100.0	336	2 T21461	hypothetical prote
16	27	100.0	346	2 A64475	hypothetical prote
17	27	100.0	367	2 C84236	hypothetical prote
18	27	100.0	372	2 BA8227	delta opioid receptor
19	27	100.0	372	2 S34592	delta opioid receptor
20	27	100.0	372	2 T38532	delta opioid receptor
21	27	100.0	373	2 T21955	hypothetical prote
22	27	100.0	376	2 A26066	segmentation prote
23	27	100.0	378	2 E83373	adenylate cyclase
24	27	100.0	387	1 S75050	IMP dehydrogenase
25	27	100.0	398	2 S74939	hypothetical prote
26	27	100.0	399	2 T18566	hypothetical prote
27	27	100.0	404	1 E0218	IMP dehydrogenase
28	27	100.0	414	1 T21954	hypothetical prote
29	27	100.0	422	2 E83083	probable two-compo

ALIGNMENTS

RESULT : 1						
T46593	Phytoene dehydrogenase [imported] - Mycobacterium marinum (fragment)	C;Species: Mycobacterium marinum	C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000	C;Accession: T46593	R;Ramakrishnan, L.; Tran, H.T.; Federpiel, N.A.; Falkow, S.	J. Bacteriol. 179, 5862-5868, 1997
A;Title: A crtB homolog essential for photochromogenicity in <i>Mycobacterium marinum</i> : 1	A;Reference number: Z23096; MUID:97440138	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Molecule type: DNA	A;Accession: T46593	A;Cross-references: EMBL:U92075; PIDN:AAB71427.1; PIDN:91928930; PIDN:91928931	A;Experimental source: strain M
C;Genetics:						
A;Gene: crtI						

Db |||||
 Db 76 GVGVP 80
 RESULT 3
 C96743 unknown protein [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C;Accession: C96743
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 616-620, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khavkin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A86141; PMID:21016719
 A;Accession: C96743
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-97 <STO>
 C;Genetics: F28P5.9
 A;Map position: 1
 Query Match 100.0%; Score 27; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No 79; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GVGVP 5
 Db 79 GVGVP 83
 RESULT 4
 S33491 hypothetical protein 6 (typel) - fowl adenovirus 1
 C;Species: Aviadenovirus gall (fowl adenovirus 1, CELO)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999
 C;Accession: S33491
 R;Akopian, T.A.; Kaverina, E.N.; Kruglyak, V.A.; Naroditsky, B.S.; Tikhonenko, T.T.
 submitted to the EMBL Data Library, May 1993
 A;Description: Sequence of an avian adenovirus (CELO) DNA fragment (11.2 - 19.2 %).
 A;Accession number: S33486
 A;Accession: S33491
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-161 <AKO>
 A;Cross references: EML:Z22864; NID:9311514; PID:CAA80482.1; PID:9311520
 C;Superfamily: fowl adenovirus 1 hypothetical protein 6
 Query Match 100.0%; Score 27; DB 2; Length 161;
 Best Local Similarity 100.0%; Pred. No 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GVGVP 5
 Db 57 GVGVP 61
 RESULT 5
 T10113 hypothetical protein - maize streak virus (isolate SP2)
 C;Species: maize streak virus
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C;Accession: T10113
 R;Ishard, M.; Granier, M.; Frutos, R.; Reynaud, B.; Peterschmitt, M.
 J. Gen. Virol. 79, 3091-3099, 1998
 A;Title: Quasispecies nature of three related maize streak virus isolates obtained th
 A;Reference number: Z16955; PMID:93094636
 A;Accession: T10113
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-206 <ISN>
 A;Cross references: EMBL:AJ225008; NID:92980718; PID:CAA12317.1; PID:92980722
 Query Match 100.0%; Score 27; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No 1.7e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GVGVP 5
 Db 128 GVGVP 132
 RESULT 6
 D64301 hypothetical protein MJ0012 - *Methanococcus jannaschii*
 C;Species: *Methanococcus jannaschii*
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 10-Oct-1997
 C;Accession: D64301
 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
 ; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Giodek,
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.O.; Woese
 C;Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*
 A;Reference number: A64300; PMID:9633799
 A;Accession: D64301
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-408 <EBUL>
 A;Cross references: GB:U67460; GB:L77117; NID:91590823; TIGR:JM0012; PI
 C;Genetics:
 A;Map position: REV14050-13424
 A;Start codon: TTG
 Query Match 100.0%; Score 27; DB 2; Length 208;
 Best Local Similarity 100.0%; Pred. No 1.7e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GVGVP 5
 Db 130 GVGVP 134
 RESULT 7
 S73791 hypothetical protein A19_ORF211 - *Mycoplasma pneumoniae* (strain ATCC 29342)
 C;Species: *Mycoplasma pneumoniae*
 A;Variety: ATCC 29342
 C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
 R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkli, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
 A;Title: Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumoniae*
 A;Reference number: S73791
 A;Accession: S73791
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-211 <HIM>
 A;Cross references: EMBL:AE000046; GB:000089; NID:91674152; PID:AB96113.1; PID:9167
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
 C;Genetics:
 A;Genetic code: SGCG3
 C;Superfamily: *Mycoplasma pneumoniae* hypothetical protein A19_ORF211

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-256 <KUN>
A;Cross-references: GB:Z99112; GB:AL009126; NID:92633902; PIDN:CRB13427.1; PID:926339
A;Experimental source: strain 168
C;Genetics:
A;Gene: PYRDII
C;Superfamily: Pyrococcus furiosus cytochrome-c3 hydrogenase gamma chain

Query Match 100.0%; Score 27; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
Db 24 GVGVP 28

RESULT 8
T23593 hypothetical protein K10H10_4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000
C;Accession: T23593
R; Percy, C.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19766
A;Accession: T23593
A;Status: preliminary; translated from GB/BMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-214 <WIL>
A;Cross-references: EMBL:283236; PIDN:CA05780.1; GSPDB:GN00020; CESP:K10H10.4
A;Experimental source: Clone K10H10
C;Genetics:
A;NP position: 2
A;Introns: 117/3
C;Superfamily: Caenorhabditis elegans hypothetical protein K10H10.4

Query Match 100.0%; Score 27; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
Db 195 GVGVP 199

RESULT 9
G39845 dihydroorotate dehydrogenase (electron transfer subunit) PyrDII - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 20-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 21-Jul-2000
R;Quinn, C.L.; Stephenson, B.T.; Switzer, R.L.
J. Biol. Chem. 266, 9113-9127, 1991
A;Title: Functional organization and nucleotide sequence of the *Bacillus subtilis* pyrDII
A;Reference number: A39845; MUID:91228016
A;Accession: G39845
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-256 <QUI>
A;Cross-references: GB:M59757; NID:94887706; PIDN:AAA21271.1; PID:g143391
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capriano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallo
Iech, J.; Harwood, C.R.; Hennaut, A.; Hilbert, H.; Kogoh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Larinnoe,
Koetter, P.; Konigstein, G.; Lohsappel, S.; Rosono, S.; Rullo, M.F.; Levine, A.; Liu, H.; Masuda, S.; Mauve
Y.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Patro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akuchi, M.; Tamashita, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yamauchi, K.; Yoshiida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033
A;Accession: D69686

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-256 <KUN>
A;Cross-references: GB:Z99112; GB:AL009126; NID:92633902; PIDN:CRB13427.1; PID:926339
A;Experimental source: strain 168
C;Genetics:
A;Gene: PYRDII
C;Superfamily: Pyrococcus furiosus cytochrome-c3 hydrogenase gamma chain

Query Match 100.0%; Score 27; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
Db 116 GVGVP 120

RESULT 10
S78063 homeobox protein Prh - chicken
C;Species: Gallus gallus (chicken)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1999
C;Accession: S78063
R;Crompton, M.R.; Bartlett, T.J.; MacGregor, A.D.; Manfioletti, G.; Buratti, E.; Gian
Nucleic Acids Res. 20, 5661-5667, 1992
A;Title: Identification of a novel vertebrate homeobox gene expressed in haematopoiet
A;Reference number: S26799; MUID:9308715
A;Accession: S78063
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-277 <CRO>
A;Cross-references: EMBL:X64711; NID:9297086; PIDN:CAA45966.1; PID:q297087
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;145-201/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 27; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
Db 15 GVGVP 199

Query Match 100.0%; Score 27; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
Db 15 GVGVP 199

RESULT 11
JC4558 viomycin kinase (EC 2.7.1.103) - Streptomyces capreolus
C;Species: capreomycin phosphotransferase; CPH protein; viomycin phosphotrans
C;Alternate names: capreomycin phosphotransferase; CPH protein; viomycin phosphotrans
C;Accession: JC4558
R;Thiara, A.S.; Cundliffe, E.
Gene 167, 121-126, 1995
A;Title: Analysis of two capreomycin-resistance determinants from *Streptomyces capreol*
A;Reference number: JC4557; MUID:96144260
A;Accession: JC4558
A;Molecule type: DNA
A;Cross-references: GB:U13078; NID:9533118; PIDN:AAA92037.1; PID:9533119
A;Experimental source: NCIMB 9801
A;Residues: 1-281 <THI>
A;Cross-references: GB:U13078; NID:9533118; PIDN:AAA92037.1; PID:9533119
A;Comment: This enzyme is a capreomycin-modifying enzyme, and it inactivates the comp
B and IIB.
C;Genetics:
A;Gene: cph
C;Keywords: phosphotransferase

Query Match 100.0%; Score 27; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; C:Species: Deinococcus radiodurans
 Qy 1 GVGV 5 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
 Db 68 GVGV 72 C:Accession: B75297
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
 , M.; Shen, M.; Yamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
 S.; Smith, H.O.; Ventner, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A73250; MUID:2003696
 A;Accession: B75292
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-308 <WHI>
 A;Cross-references: GB:AE002061; GB:AE000513; PIDN:AAFF1841.1; PID:9646
 A;Experimental source: strain R1
 C;Genetics:
 A;Map type: 1
 C;Superfamily: glucose kinase; glucose kinase homology <SKH>
 F:67-201/Domain: glucose kinase homology <SKH>

Query Match 100.0%; Score 27; DB 2; Length 308;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGV 5 C:Species: Caenorhabditis elegans
 Db 71 GVGV 75 C:Accession: T21461; T21709
 R;Wilkinson, J.
 Submitted to the EMBL Data Library, March 1995
 A;Reference number: Z19425
 A;Accession: T21461
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-336 <WIL>
 A;Cross-references: EMBL:Z48582; PIDN:CAA88468.1; GSDB:GN00020; CESPP:F27E5.2
 A;Experimental source: clone F27E5
 A;Submitted to the EMBL Data Library, March 1995
 A;Reference number: Z19462
 A;Accession: T21709
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-336 <WIL>
 A;Cross-references: EMBL:Z48783; PIDN:CAA88702.1; GSDB:GN00020; CESPP:F27E5.2
 A;Experimental source: clone F33H1
 C;Genetics:
 A;Gene: CESPP:F27E5.2

Query Match 100.0%; Score 27; DB 2; Length 336;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGV 5 C:Species: Mycobacterium tuberculosis (strain H37RV)
 Db 153 GVGV 157 C:Accession: F70693
 C;Species: Mycobacterium tuberculosis
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C:Accession: F70693
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
 Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
 Rajandream, M.A.; Rogers, J.; Rutte, S.; Seeger, K.; Shelton, S.; Squares, S.;
 Nature 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; MUID:98295987
 A;Accession: F70693
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-303 <COL>
 A;Cross-references: GB:Z81331; GB:AL123456; PIDN:CAB03651.1; PID:91648885
 A;Experimental source: strain H37RV
 C;Genetics:
 A;Gene: ugpA
 C;Superfamily: inner membrane protein ugpA

Query Match 100.0%; Score 27; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGV 5 C:Species: paired box transcription factor Pax-4; homeobox homology; paired box h
 Db 141 GVGV 145 C:Accession: B75292
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:13-138/Domain: paired box homology <PBH>

Query Match 100.0%; Score 27; DB 2; Length 336;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed Jul 25 16:58:03 2001

us-09-251-638-2.rpr

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Search completed: July 25, 2001, 16:50:27
Job time: 98 sec

Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5	homo sapien	Q92545		
1 protein - protein search, using sw model					
Run on:	July 25, 2001, 16:51:25 ; Search time 12.69 seconds (without alignments) 13.497 Million cell updates/sec				
Title:	US-09-251-638-2				
Perfect score:	27				
Sequence:	1 GVGVP 5				
Scoring table:	BLOSUM62				
Gapopen:	10.0 , Gapext 0.5				
Searched:	93435 seqs, 34255486 residues				
Total number of hits satisfying chosen parameters:	93435				
Minimum DB seq length: 0					
Maximum DB seq length: 2000000000					
Post-processing: Minimum Match 0%					
Maximum Match 100%					
Listing first 45 summaries					
Database :	SwissProt_39;*				
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	84	1 IG2R_HUMAN	p09565 homo sapien
2	27	100.0	208	1 YO12_METJA	p09328 methanococcus
3	27	100.0	211	1 YD71_MYCPN	p75410 mycoplasma
4	27	100.0	228	1 OPRD_PIG	p79291 sus scrofa
5	27	100.0	256	1 PYFK_BACST	p25983 bacillus su
6	27	100.0	277	1 HMPH_CHICK	Q05502 gallus gall
7	27	100.0	291	1 YA7Q_RHTSN	Q53192 rhizobium s
8	27	100.0	372	1 OPRD_HUMAN	P41143 homo sapien
9	27	100.0	372	1 OPRD_MOUSE	P32300 mus musculu
10	27	100.0	372	1 OPRD RAT	P33533 rattus norv
11	27	100.0	376	1 RMEV_DROME	P06602 drosophila hu
12	27	100.0	404	1 IMDH_BORBU	P49058 borrelia hu
13	27	100.0	477	1 ME12_HUMAN	Q14770 homo sapien
14	27	100.0	477	1 MET2_MOUSE	P97367 mus musculu
15	27	100.0	485	1 IMDH_PYRFU	P42851 pyrococcus
16	27	100.0	486	1 IMDH_PYRHO	Q58045 pyrococcus
17	27	100.0	488	1 IMDH_ECOLIJ	P06781 escherichia
18	27	100.0	488	1 IMDH_HAFTN	P44334 haemophilus
19	27	100.0	490	1 IMDH_AQUAE	Q67820 aquifex aeo
20	27	100.0	492	1 IMDH_STPRTY	P50999 streptococc
21	27	100.0	496	1 IMDH_MENJA	P59011 methanococc
22	27	100.0	507	1 CRTI_STPRGR	P54981 streptomyce
23	27	100.0	507	1 DAF_CAVPO	P54971 streptomyce
24	27	100.0	508	1 CRTI_STPSE	P54970 streptomyce
25	27	100.0	513	1 IMDH_BACSU	P21879 bacillus su
26	27	100.0	635	1 CA18_HUMAN	P25067 homo sapien
27	27	100.0	684	1 FLUD_HELPPY	P96786 helicobacte
28	27	100.0	730	1 ELS_HUMAN	P15502 homo sapien
29	27	100.0	747	1 ELS_BOVIN	P04985 bos taurus
30	27	100.0	747	1 YNS4_CAFTEL	P34588 caenorhabdi
31	27	100.0	750	1 ELS_CHICK	P07916 gallus gall
32	27	100.0	758	1 TX1_XENIA	P14380 xenopus lae
33	27	100.0	1758	1 CAYA_CAFTEL	P17146 caenorhabdi
34	27	100.0	1805	1 RWL_HUMAN	P26778 bacillus li
35	27	100.0	1829	1 RWL_MOUSE	P32727 bacillus st
36	27	100.0	2944	1 CA17_HUMAN	P05324 mycobacteri
37	26	96.3	65	1 Y12J_BPT4	P09153 escherichia
38	26	96.3	125	1 KC1A_PIG	Q47472 escherichia
39	26	96.3	139	1 HMAA_ARTSF	
40	26	96.3	146	1 SP22_BACLI	
41	26	96.3	146	1 SP22_BACST	
42	26	96.3	198	1 LEUD_MYCUL	
43	26	96.3	198	1 LEUD_MYCTU	
44	26	96.3	200	1 TFAE_ECOLI	
45	26	96.3	203	1 TFAB_ECOLI	
				ALIGNMENTS	
				RESULT 1	
				IG2R_HUMAN	
				STANDARD;	
				PRT;	84 AA.
				RP	
				SEQUENCE FROM N.A.	
				RC	TISSUE=Placenta;
				RX	Medline=89000779; PubMed=3167054;
				RA	de Pagter-Holtluizen P., van der Kammen R.A., Jansen M.,
				RA	van Schaik F.M.A., Sussenbach J.S.;
				RT	"Different expression of the IGF-II mRNAs and an mRNA encoding a putative IGF-II-associated protein."
				RT	Gene Characterization of the IGF-II mRNAs and an mRNA encoding a putative IGF-II-associated protein.";
				RL	Biochim. Biophys. Acta 950:282-295(1988).
				CC	-1 FUNCTION NOT KNOWN.
				CC	-1 MISCELLANEOUS: THE COORDINATED EXPRESSION OF INSULIN-LIKE GROWTH FACTOR (IGF II) ASSOCIATED PROTEIN AND IGF II IS DEVELOPMENTALLY AND TISSUE-SPECIFICALLY REGULATED.
				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announces or send an email to license@isb-sib.ch).
				CC	EMBL: X07868; CAR30718.1; -.
				DR	DR PTR; S03384; S03384.
				KW	Growth factor
				SQ	SEQUENCE 84 AA; 9081 MW; 8BFBB4E49EE5EFAB CRC64;
				Qy	Query Match 100.0%; Best Local Similarity 100.0%; Matches 5; Conservative 0; Indels 0; Gaps 0;
				Db	76 GVGP 5
				RESULT 2	
				Y012_METJA	
				STANDARD;	
				ID Y012_METJA	
				AC Q80328;	
				RESIDUE 2	
				01-NOV-1997	
				Rel. 35	
				Created)	
				Pei 35	Last sequence update
				Pei 35	

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE HYPOTHETICAL PROTEIN MJ0012;

GN MJ0012.

OS Methanococcus jannaschii.

OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;

OC Methanococcus.

NCBI_TaxID=2190;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

RX MEDLINE=96337999; PubMed=868087;

RA Built C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

RA Kerlavage A.R., Blattner R.F., Fitzgerald L.M., Tomb J.F., Adams M.D., Reich C.T.,

RA Overbeek R., Kirkness E.F., Dougherty B.A., Merrick J.M., Glodek A.,

RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

RA Utterback T.R., Kelley J.M., J.D., Sodjo P.W., Hanna M.C.,

RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

RA Klener H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

RT "Complete genome sequence of the methanogenic archaeon, Methanococcus

jannaschii.";

RT Science 273:1058-1073(1996).

CC -I SIMILARITY: STRONG, TO THE C TERMINAL OF M.JANNASCHII MJ1635.

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CC or send an email to license@isb-sib.ch).

DR EMBL; 067460; - ; NOT_ANNOTATED_CDS.

DR TIGR; MJ0012; - .

KW Hypothetical protein.

SQ SEQUENCE 208 AA; 24347 MW; 4C824F93015561B4 CRC64;

RP Hypothetical protein.

CC 208 AA; 24347 MW; 4C824F93015561B4 CRC64;

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CC or send an email to license@isb-sib.ch).

DR EMBL; 071149; AB36964.1; - .

DR GCRDb; GCR_1526; - .

DR InterPro; IPR00276; - .

DR Pfam; PF00001; 7tm_1; 1.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS5062; G_PROTEIN_RECEP_F1_2; 1.

DR G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Phosphorylation; Lipoprotein; Palmitate.

FT NON_TER 1 1 1 (POTENTIAL).

FT TRANSMEM <1 3 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 4 12 2 (POTENTIAL).

FT TRANSMEM 13 30 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 31 52 3 (POTENTIAL).

FT TRANSMEM 53 72 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 73 102 4 (POTENTIAL).

FT TRANSMEM 103 118 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 119 143 5 (POTENTIAL).

FT TRANSMEM 144 166

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CC or send an email to license@isb-sib.ch).

CC EMBL; AE000046; AAB96113.1; - .

KW Hypothetical Protein.

SEQUENCE 211 AA; 23592 MW; A5E240288852DDB2 CRC64;

SQ

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Score 27; DB 1; Length 211; (Rel. 40, Created)

Score 27; DB 1; Length 211; (Rel. 40, Last sequence update)

Score 27; DB 1; Length 211; (Rel. 40, Last annotation update)

Score 27; DB 1; Length 211; (Rel. 40, Last annotation update)

Score 27; DB 1; Length 211; (Rel. 40, Last annotation update)

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Score 27; DB 1; Length 211; (Rel. 40, Last annotation update)

Score 27; DB 1; Length 211; (Rel. 40, Last annotation update)

Score 27; DB 1; Length 211; (Rel. 40, Last annotation update)

Score 27; DB 1; Length 211; (Rel. 40, Last annotation update)

Score 27; DB 1; Length 211; (Rel. 40, Last annotation update)

Query Match 100.0%; Score 27; DB 1; Length 228;
 Best Local Similarity 100.0%; Pred. No. 74; Length 256;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
 |||||
 Db 106 GVGVP 110

RESULT 5
 PARK_BACSU
 ID PARK_BACSU STANDARD PRT; 256 AA.
 AC P25983;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE DIHYDROOROTATE DEHYDROGENASE ELECTRON TRANSFER SUBUNIT.
 GN PYRD OR PYRZ OR PYRD2 OR PYRDII.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN [1];
 RN NCBI_TaxID=9031;
 RN [1];
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91225016; PubMed=11709162;
 RA Quinn C.L., Stephenson B.T., Switzer R.L.;
 RT "Functional organization and nucleotide sequence of the Bacillus
 subtilis Pyrimidine biosynthetic operon.";
 RI J. Biol. Chem. 266:9113-9127(1991).
 RN [2];
 RP STRAIN=168 / DB104;
 RX MEDLINE=96336349; PubMed=8759868;
 RA Kahler A.E., Switzer R.L.;
 RT "Identification of a novel gene of Pyrimidine nucleotide
 biosynthesis, pyrdI, that is required for dihydroorotate
 dehydrogenase activity in *Bacillus subtilis*.";
 RI J. Bacteriol. 178:5013-5016(1996).
 RN [3];
 RP CHARACTER=10545205;
 RX MEDLINE=20014515; PubMed=10545205;
 RA Kahler A.E., Nielsen F.S., Switzer R.L.;
 RT "Biochemical characterization of the heteromeric *Bacillus subtilis*
 dihydroorotate dehydrogenase and its isolated subunits.";
 RI Arch. Biochem. Biophys. 371:191-201(1999).
 CC -I- FUNCTION: PROBABLE ELECTRON CARRIER PROTEIN INVOLVED IN THE
 TRANSFER OF REDUCING EQUIVALENTS FROM THE FLAVOPROTEIN SUBUNIT
 (PYRD) TO THE ELECTRON TRANSPORT SYSTEM IN THE CELL MEMBRANE.
 CC -I- COFACTOR: BINDS A 2FE-2 CLUSTER AND FAD.
 CC -I- PATHWAY: FOURTH STEP IN PYRIMIDINE BIOSYNTHESIS.
 CC -I- SUBUNIT: HETEROOTERAMER OF 2 PYRK AND 2 PYRD SUBUNITS.
 CC -I- SIMILARITY: BELONGS TO THE PYRK FAMILY.

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CC DR; M59757; AAA21271.1; -;
 DR EMBL; 299112; CAB3427.1; -;
 DR PIR; G39845; G39845.

DR Subtilist; BG10717; PYRF.
 KW Pyrimidine biosynthesis; Electron transport; Iron-sulfur;
 KW Flavoprotein; FAD.

FT FAD (POTENTIAL).
 KW IRON-SULFUR (2FE-2S) (PROBABLE).
 NP-BIND 110 122
 FT IRON-SULFUR (2FE-2S) (PROBABLE).
 METAL 220 225
 FT IRON-SULFUR (2FE-2S) (PROBABLE).
 METAL 228 228
 FT IRON-SULFUR (2FE-2S) (PROBABLE).
 METAL 243 243
 SQ SEQUENCE 256 AA; 28099 MW; DC:BG760539C2815 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 256;
 Best Local Similarity 100.0%; Pred. No. 82; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
 |||||
 Db 116 GVGVP 120

RESULT 6
 HMPH_CHICK STANDARD PRT; 277 AA.
 ID HMPH_CHICK
 AC Q05502;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE HOMEOBOX PROTEIN PRH.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN NCBI_TaxID=9031;

RN [1];
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93087-75; PubMed=1360645;
 RA Crompton M.R., Bartlett T.J., Macgregor A.D., Manfioletti G.,
 RA Buratti E., Giancotti V., Goodwin G.H.;
 RT "Identification of a novel vertebrate homeobox gene expressed in
 RT hematopoietic cells".
 RL Nucleic Acids Res. 20:5561-5567 (1992).
 CC -I- FUNCTION: RECOGNIZES THE DNA SEQUENCE 5'-ATTTAA-3'. MAY PLAY A ROLE
 CC IN HEMATOPOIETIC DIFFERENTIATION
 CC -I- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
 CC -I- TISSUE SPECIFICITY: IN ALL HEMATOPOIETIC TISSUES EXCEPT
 CC PERIPHERAL BLOOD ERYTHROCYTES AND IN THE LIVER AND LUNG.
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 CC or send an email to license@isb-sib.ch).
 CC DR EMBL; X64711; CAAJ5966.1; -.
 DR HSSP; P22808; 1VND.
 DR InterPro; IPR001356; -.
 DR Pfam; PF00046; homeobox; 1.
 DR PRNTS; PR00024; HOMEBOX.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein.
 FT DOMAIN 1 140
 FT DNA_BIND 144 203
 SQ SEQUENCE 277 AA; 30213 MW; BE744C143FB99FC CRC64;

Query Match 100.0%; Score 27; DB 1; Length 277;
 Best Local Similarity 100.0%; Pred. No. 89; Mismatches 0; Indels 0; Gaps 0;

Query 1 GVGVP 5
 Db 178 GVGVP 182
 SEQUENCE FROM N.A.
 MEDLINE=93110361; PubMed=1334555;
 RA Kieffer B.L., Befort K., Gaveriaux-Ruff C., Hirth C.G.;
 RT "Cloning of a delta opioid receptor: isolation of a cDNA by expression cloning and pharmacological characterization";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:12048-12052(1992).
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain;
 RX MEDLINE=93442064; PubMed=8393575;
 RA Yasuda K., Raynor K., Kong H., Bredre C.D., Takeda J., Reisine T.,
 RA Bell G.T.;
 RT "Cloning and functional comparison of kappa and delta opioid receptors from mouse brain";
 RT Proc. Natl. Acad. Sci. U.S.A. 90:6736-6740(1993).
 RL [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93291482; PubMed=8397421;
 RA Keith D.E. Jr., Anton B., Evans C.J.;
 RT "Characterization and mapping of a delta opioid receptor clone from NG108-15 cells";
 RT Proc. West. Pharmacol. Soc. 36:299-306(1993).
 RN [5]
 SEQUENCE OF 8-372 FROM N.A.

Query 1 GVGVP 5
 Db 178 GVGVP 182
 SEQUENCE FROM N.A.
 MEDLINE=94022364; PubMed=8415697;
 RA Bzdega T., Chin H., Kim K., Jung H.H., Kozak C.A., Klee W.A.;
 RT "Regional expression and chromosomal localization of the delta opiate receptor gene";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:9305-9309(1993).
 RN [6]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=97001837; PubMed=8844829;
 RA Alford I., Loew G.H.;
 RT "A 3D model of the delta opioid receptor and ligand-receptor complexes";
 RT Protein Eng. 9:573-583(1996).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM ION CURRENTS AND INCREASING POTASSIUM CONDUCTANCE. HIGHLY STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN, WITH HIGH CONCENTRATIONS IN THE BASAL GANGLIA AND LIMBIC REGIONS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

Query Match 100.0%; Score 27; DB 1; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GVGVP 5
 Db 178 GVGVP 182

RESULT 9
 ORD_MOUSE
 ID P32300; STANDARD; PRT; 372 AA.
 AC DT 01-OCT-1993 (Rel. 27, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (K56) (MSL-2).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TAXID=10090.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93110361; PubMed=1334555;
 RA Kieffer B.L., Befort K., Gaveriaux-Ruff C., Hirth C.G.;
 RT "Cloning of a delta opioid receptor: isolation of a cDNA by expression cloning and pharmacological characterization";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:12048-12052(1992).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93110361; PubMed=1335167;
 RA Evans C.J., Keith D.E. Jr., Morrison H., Magendzo K., Edwards R.H.;
 RT "Cloning of a delta opioid receptor by functional expression.";
 RL Science 258:1952-1955(1992).
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain;
 RX MEDLINE=93442064; PubMed=8393575;
 RA Yasuda K., Raynor K., Kong H., Bredre C.D., Takeda J., Reisine T.,
 RA Bell G.T.;
 RT "Cloning and functional comparison of kappa and delta opioid receptors from mouse brain";
 RT Proc. Natl. Acad. Sci. U.S.A. 90:6736-6740(1993).
 RL [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93291482; PubMed=8397421;
 RA Keith D.E. Jr., Anton B., Evans C.J.;
 RT "Characterization and mapping of a delta opioid receptor clone from NG108-15 cells";
 RT Proc. West. Pharmacol. Soc. 36:299-306(1993).
 RN [5]
 SEQUENCE OF 8-372 FROM N.A.

Query Match	100.0%	Score 27; DB 1; Length 372;					
Best Local Similarity	100.0%	Pred. No. 1.2e+02;					
Matches	5; Conservative	0; Mismatches 0;	Indels 0;	Gaps 0;			
Qy	1 GVGVP 5						
Db	178 GVGVP 182						
RESULT 10							
OPRD_RAT	ID	OPRD_RAT STANDARD; PRT; 372 AA.					
AC	P35333; P35333;	Rel. 28; Created)					
DT	01-FEB-1994 (Rel. 28; Last sequence update)						
DT	01-NOV-1997 (Rel. 35; Last annotation update)						
DE	DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).						
GN	OPRD1 OR ROR-A.						
OS	Rattus norvegicus (Rat).						
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Metazoa; Sciuromorpha; Muridae; Murinae; Rattus.						
OX	NCBI_TAXID=10116;						
RN	{1}						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Brain;						
RX	MEDLINE=93351652; PubMed=8394245;						
RA	Fukuda K., Kato S., Mori K., Nishi M., Takeshima H.; "Primary structures and expression from cDNAs of rat opioid receptor delta- and mu-subtypes"; FEBS Lett. 327:311-314(1993);						
RT	[2]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;						
RX	MEDLINE=94322412; PubMed=7519274;						
RA	Abed M.E., Noel M.A., Farnsworth J.S., Tao Q.; "Molecular cloning and expression of a delta-opioid receptor from rat brain"; J. Neurosci. Res. 37:714-719(1994).						
RT	[3]						
CC	-I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY STEREOSELECTIVE RECEPTOR FOR ENKEPHALINS.						
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.						
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.						
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).						
CC	[4]						
DR	EMBL: D16348; BAA03851.1; -;						
DR	EMBL: U00475; AAA19939.1; -;						
DR	PIR: S34592; S34592; -;						
DR	GCRDb; GCR_0805; -;						
DR	InterPro; IPR000226; -;						
DR	InterPro; IPR00031; -;						
DR	InterPro; IPR001418; -;						
DR	Pfam; PF00001; 7tm_1; 1;						
DR	PRINTS; PR00237; GPCRHDOPPSN.						
DR	PRINTS; PR00284; OPIOUDR.						
DR	PRINTS; PR00252; DELTAPTOIN.						
DR	PROSITE; PS00237; G-PROTEIN RECEP_F1_1; 1.						
DR	PROSITE; PS50262; G-PROTEIN RECEP_F1_2; 1.						
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;						
KW	Phosphorylation; Lipoprotein; Palmitate.						
FT	DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).						
FT	TRANSMEM 46 75 1 (POTENTIAL).						
FT	CYTOSMIC (POTENTIAL).						
FT	TRANSMEM 76 84 2 (POTENTIAL).						
FT	TRANSMEM 85 102 2 (POTENTIAL).						
FT	DOMAIN 103 124 EXTRACELLULAR (POTENTIAL).						
FT	TRANSMEM FT DOMAIN 125 144 3 (POTENTIAL).						
FT	TRANSMEM FT DOMAIN 145 174 CYTOPLASMIC (POTENTIAL).						
FT	TRANSMEM FT DOMAIN 175 190 4 (POTENTIAL).						
FT	TRANSMEM FT DOMAIN 191 215 EXTRACELLULAR (POTENTIAL).						
FT	TRANSMEM FT DOMAIN 216 238 5 (POTENTIAL).						
FT	TRANSMEM FT DOMAIN 239 261 CYTOPLASMIC (POTENTIAL).						
FT	TRANSMEM FT DOMAIN 262 284 6 (POTENTIAL).						
FT	TRANSMEM FT DOMAIN 285 293 EXTRACELLULAR (POTENTIAL).						
FT	TRANSMEM FT DOMAIN 294 310 7 (POTENTIAL).						
FT	TRANSMEM FT DOMAIN 311 372 CYTOPLASMIC (POTENTIAL).						
FT	TRANSMEM FT DOMAIN 318 18 N-LINKED (GLCNAC. . .) (POTENTIAL).						
FT	CARBHYD FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).						
FT	DISULFID FT DISULFID 121 198 BY SIMILARITY.						
FT	LIPID FT LIPID 333 333 PALMITATE (POTENTIAL).						
SQ	SEQUENCE 372 AA; 40449 MW; F575BD1F4C6D50 CRC64;						
Query Match	100.0%	Score 27; DB 1; Length 372;					
Best Local Similarity	100.0%	Pred. No. 1.2e+02;					
Matches	5	Conservative 0; Mismatches 0;	Indels 0;	Gaps 0;			
PRT	1 GVGVP 5						
Db	178 GVGVP 182						
RESULT 11							
HMEV_DROME	ID HMEV_DROME STANDARD; PRT; 376 AA.						
ID	P06602; P07667; Q9Y5E6;						
AC	01-FAN-1988 (Rel. 06; Created)						
DT	01-OCT-2000 (Rel. 40; Last sequence update)						
DT	01-OCT-2000 (Rel. 40; Last annotation update)						
DE	SEGMENTATION PROTEIN EVEN-SKIPPED.						
GN	EVE OR CG2328						
OS	Drosophila melanogaster (Fruit fly).						
OC	Eukaryota; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydioidea; Dirosophilidae; Drosophila.						
OC	NCB_TAXID=7277;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=8/05144; PubMed=287745;						
RA	McDonald P.M.; Ingham P.; Struhl G.; RT "Isolation, structure, and expression of even-skipped: a second pair-rule gene of Drosophila containing a homeo box.";						
RA	Frassetto M.; Hoey T.; Ruschow C.; Doyle B.; Levine M.; RT Characterization and localization of the even-skipped protein of Drosophila.";						
RL	[2]						
RN	SEQUENCE FROM N.A.						
RX	MEDLINE=8/21836; PubMed=2884106;						
RA	Frasch M.; Hoey T.; Ruschow C.; Doyle B.; Levine M.; RT Characterization and localization of the even-skipped protein of Drosophila.";						
RL	[3]						
RN	SEQUENCE FROM N.A.						
RC	STRAIN=BERKELEY;						
RX	MEDLINE=2019606; PubMed=10731132;						
RA	Adams M.D.; Celinker S.E.; Holt R.A.; Gocayne J.D., RA Amatiades P.G.; Scherer S.E.; Li P.W.; Hostkin R.A.; Galle R.F., RA George R.A.; Lewis S.E.; Richards S.; Ashburner M.; Henderson S.N., RA Sutton G.G.; Wortman J.R.; Yandell M.D.; Zhang Q.; Chen L.X., RA Brandon R.C.; Rogers Y.-H.C.; Blasius R.G.; Champe M.; Pfeiffer R.D., RA Wan K.H.; Doyle C.; Baxter E.G.; Heit G.; Nelson C.R.; Miklos G.L.G., RA Abril J.J.F.; Agbayani C.; An H.-J.; Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M.; Basu A.; Baxendale J.; Bayraktaroglu L.; Beasley E.M., RA Beeson K.Y.; Benos P.V.; Berman B.P.; Bhandari D.; Bolashakov S., RA Borkova D.; Botchan M.R.; Bouck J.; Brokstone P.; Brottier P., RA Burtsik K.C.; Busam D.A.; Butler J.; Cadile E.; Center A.; Chandra I., RA Cherry J.M.; Cowley S.; Dahlke C.; Davenport L.B.; Davies P., RA de Pablo B.; Delcher A.; Deng Z.; Mays A.D.; Dew I.; Dietz S.M., RA Dodson K.; Doup L.E.; Downes M.; Dugan-Rocha S.; Dunkov B.C.; Dunn P., RA Durbin R.J.; Doup L.E.; Ferriera S.; Fleischmann W., RA						

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CC EMBL; U13372; AAA3247.1; -
 CC DR EMBL; AE000792; AAC66314.1; -
 CC DR TIGR; BBP17; -
 CC DR PDB; 1EEP; 29-MAR-00;
 CC InterPro; IPR01033; -
 CC Pfam; PF00478; IMDH_C; 1.
 CC DR Pfam; PF01574; IMDH_N; 1.
 CC PROSITE; PS00087; IMP_DH_GMP_RED; 1.
 CC KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Plasmid;
 CC KW 3D-structure; 3D-structure.
 CC FT BINDING; 229 IMP.
 CC SQ SEQUENCE 404 AA; 43767 MW; A91D6DC5CE322F1 CRC64;

Query Match 100.0% Score 27; DB 1; Length 404;
 Best Local Similarity 100.0% Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVGVYP 5
 Db 236 GVGVYP 240

RESULT 13
 MEI2_HUMAN STANDARD; PRT; 477 AA.

AC O14770; Q9NR3; Q9NRS2; Q9NS1;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HOMEBOX PROTEIN MEI2 (MEIS1-RELATED PROTEIN 1).
 GN MEI2 OR MRG1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrini; Homidae; Homo.
 NCBI_TAXID=9606;

RN 1
 RP SEQUENCE FROM N.A. (ISOFORMS MEIS2C; MEIS2D AND MEIS2E).
 RC TISSUE=TRAIT;
 RT "Three-amino acid extension loop homeodomain proteins Meis2 and TGIF
 differentially regulate transcription.";
 RL J. Biol. Chem. 275:20734-20741(2000).
 RN [2]

RP SEQUENCE OF 271-477 FROM N.A. (ISOFORM MEIS2B).
 RX MEDLINE=98051942; PubMed=9183298;
 RA Wang C.R., D'Souza U.M., Lee S.-H., Junn E., Mouradian M.M.,
 RT "Chromosomal mapping to 15q14 and expression analysis of the human
 MEIS2 homeobox gene.";
 RL Mamm. Genome 8:951-952(1997).

CC 1 - SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
 CC -1 - ALTERNATIVE PRODUCTS: 5 ISOFORMS; MEIS2A, MEIS2C (SHOWN
 HERE), MEIS2D AND MEIS2E; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1 - TISSUE SPECIFICITY: EXPRESSED IN VARIOUS TISSUES. IN HEMATOPOIETIC
 CC TISSUES, THE LYMPHOID ORGANS EXPRESS HIGH LEVELS OF MEIS2. ALSO
 CC EXPRESSED IN SOME REGIONS OF THE BRAIN, SUCH AS THE PUTAMEN.

CC -1 - SIMILARITY: BELONGS TO THE TALE/MEIS FAMILY OF HOMEBOX PROTEINS.

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 CC or send an email to license@isb-sib.ch).

CC DR AF179897; AAF81640.1; -
 CC DR AF179898; AAF81641.1; -

DR EMBL; AF179899; AAF81642.1; -
 DR EMBL; AF017418; AAB70270.1; -
 DR InterPro; IPR01356; -
 DR MIM; 601740; -
 DR Prosite; PS0027; HOMEobox_2; 1.
 DR PROSITE; PS50071; HOMEobox_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein; Alternative splicing.
 FT DOMAIN 195 244 SER/THR-RICH (ACIDIC).
 FT DOMAIN 246 273 ASP/GLU-RICH (ACIDIC).
 DR POLY ASP.
 DR HOMEBOX (TALE-TYPE).
 DR MISSING (IN ISOFORM MEIS2B AND ISOFORM
 MEIS2D).
 DR HP -> VV (IN ISOFORM MEIS2E).
 DR MISSING (IN ISOFORM MEIS2E).
 DR LQSMGDYVSGGPAGMS -> PMSSMGANGMDGGWHYM
 DR (IN ISOFORM MEIS2A AND ISOFORM MEIS2B).
 DR MISSING (IN ISOFORM MEIS2A AND ISOFORM
 MEIS2B).
 DR 94BBD0801A312B24 CRC64;

Query Match 100.0% Score 27; DB 1; Length 477;
 Best Local Similarity 100.0% Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVGVYP 5
 Db 16 GVGVYP 20

RESULT 14
 MEI2_MOUSE
 ID MEI2_MOUSE STANDARD; PRT; 477 AA.
 AC P97167; Q35676; P07403; O35677; P97404;
 DT 15-DEC-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE HOMEBOX PROTEIN MEI2 (MEIS1-RELATED PROTEIN 1).
 GN MEI2 OR MRG1 OR STRA10
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TAXID=10090;

RN 1
 RP SEQUENCE FROM N.A. (ISOFORM MEIS2A).
 RC SWISS WEBSTER;
 RX MEDLINE=57108670; PubMed=8950991;
 RA Nakamura T., Jenkins N.A., Copeland N.G.;
 RA "Identification of a new family of Pbx-related homeobox genes."
 RN [1]
 OS Mus musculus (Mouse).
 OC Mus musculus (Mouse).
 OC Murinae; Muridae; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBITaxonID=10090;

RN 2
 RP SEQUENCE FROM N.A. (ISOFORM MEIS2A; MEIS2C AND MEIS2D).
 RC SWISS WEBSTER;
 RX MEDLINE=97477074; PubMed=9337137.
 RA Oulad-Abdelghani M., Chazaud C., Bouillet P., Sapin V., Chambon P.,
 RA Doille P.;
 RA "A novel mouse Pbx-related homeobox gene induced by retinoic
 acid during differentiation of P19 embryonal carcinoma cells.";
 RT Dev. Dyn. 210:173-183(1997).
 RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS MEIS2B/MRG1 AND MEIS2D/MRG1B).
 RX MEDLINE=9720105; PubMed=9049632;
 RA Steelman S., Mostow J.J., Muzynski K., North C., Druck T.,
 RA Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.;
 RT "Identification of a conserved family of Meis1-related homeobox
 genes."
 RT Genom. Res. 7:142-156(1997).

CC 1 - SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
 CC -1 - ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS: MEIS2A,
 CC MEIS2B/MRG1A, MEIS2C (SHOWN HERE) AND MEIS2D/MRG1B; ARE PRODUCED
 CC BY ALTERNATIVE SPLICING.
 CC -1 - TISSUE SPECIFICITY: DISPLAYS SPATIALLY RESTRICTED EXPRESSION
 CC PATTERNS IN THE DEVELOPING NERVOUS SYSTEM, LIMBS, FACE, AND IN

CC VARIOUS VISCERA. IN ADULT, IT IS MAINLY EXPRESSED IN THE BRAIN AND
 CC FEMALE GENITAL TRACT, WITH A DIFFERENT DISTRIBUTION OF THE
 CC ALTERNATIVE SPLICE FORMS IN THESE ORGANS. LOWER EXPRESSION IN LUNG
 CC AND ONLY BASAL LEVEL IN HEART, LIVER, KIDNEY, SPLEEN, AND TESTIS.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN ALL STAGES OF
 CC EMBRYONIC DEVELOPMENT ANALYSED (7 DAYS TO 17 DAYS).
 CC -!- INDUCTION: BY RETINOIC ACID.
 CC -!- SIMILARITY: BELONGS TO THE TALE/MEIS FAMILY OF HOMEOBOX PROTEINS.

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DR EMBL; U57343; AAC52948.1; -;
 DR EMBL; AJ000504; CAA04138.1; -;
 DR EMBL; AJ000505; CAA04139.1; -;
 DR EMBL; AJ000506; CAA04140.1; -;
 DR EMBL; AJ000507; CAA04141.1; -;
 DR EMBL; U68383; AAB19193.1; -;
 DR EMBL; U68384; AAB19194.1; -;
 DR MGD; MGI:108564; Mr91.
 DR InterPro; IPR001356.
 DR PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
 DR PROSITE; PS50071; HOMEOBOX_2; 1.
 KW DNA-binding; Nucleic acid binding protein; Homeobox; Alternative splicing.
 FT DOMAIN 195 244 SER/THR RICH.
 FT DOMAIN 246 273 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 266 273 POLY-ASP.
 FT DNA_BIND 276 338 HOMEBOX (TALE-TYPE).
 FT VARSPLIC 346 352 MISSING (IN ISOFORM MEIS2B AND ISOFORM MEIS2D).
 FT VARSPLIC 384 401 LOSMPGDDVSQGGPMGNG > PMSGNGNMGMGQWYHM.
 FT VARSPLIC 402 477 (IN ISOFORM MEIS2A AND ISOFORM MEIS2B).
 FT VARSPLIC 477 51728 MW; MISSING (IN ISOFORM MEIS2A AND ISOFORM MEIS2B).
 FT CONFLICT 2 2 A -> E (IN REF. 1).
 FT CONFLICT 316 316 T -> A (IN REF. 1).
 SQ SEQUENCE 477 AA; 9236108008647A21 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 477;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;

Qy 1 GVGVP 5
 Db 16 GVGVP 20

RESULT 15

IMDH_PYRFU
 ID IMDH_PYRFU
 AC P42851;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205) (IMP
 DE DEHYDROGENASE) (IMPDH) (IMPDH).
 GN GUAB.
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 OX NCBI_TAXID:2261;

RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=97045814; PubMed=8890736;
 RA Collart F.R., Ospipuk J., Trent J., Olsen G.J., Huberman E.;
 RT Cloning, characterization and sequence comparison of the gene coding
 RT for IMP dehydrogenase from Pyrococcus furiosus.";
 RL Gene 174:209-216(1996).

Search completed: July 25, 2001, 16:51:26
 Job time: 157 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 25, 2001, 16:51:06 ; Search time 33.32 Seconds
(without alignments)
19.854 Million cell updatess/sec

Title: US-09-251-638-2
Perfect score: 27
Sequence: 1 GVGVP 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_16:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rabbit:
 12: sp_unclassified:
 13: sp_vertebrate:
 14: sp_virus:
 Listing first 45 summaries

SPTREMBL_16:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rabbit:
 12: sp_unclassified:
 13: sp_vertebrate:
 14: sp_virus:
 Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	27	100.0	38	2	005422		005422 mycobacteri
2	27	100.0	88	2	09RFV0		Q9RFV0 renibacteri
3	27	100.0	88	2	09R222		Q9R222 renibacteri
4	27	100.0	95	14	09DSW9		Q9DSW9 ascovirus d
5	27	100.0	153	2	09ZU16		Q9ZU16 helicobacte
6	27	100.0	161	14	064178		Q64178 avian adeno
7	27	100.0	178	3	P78931		P78931 schizosacch
8	27	100.0	206	14	056970		Q56970 maize strea
9	27	100.0	206	14	073468		Q73468 maize strea
10	27	100.0	206	14	073472		Q73472 maize strea
11	27	100.0	206	14	073474		Q73474 maize strea
12	27	100.0	206	14	083476		Q83476 maize strea
13	27	100.0	214	5	045681		Q45681 caenorhabdi
14	27	100.0	223	5	09KTY0		Q9KTY0 streptomyce
15	27	100.0	240	13	09DDR8		Q9DDR8 gallus gall
16	27	100.0	246	2	Q8EX74		Q9EX74 rhodococcus
17	27	100.0	256	4	Q9RF54		Q9RF54 oryza sativ
18	27	100.0	258	4	Q9UNF5		Q9UNF5 homo sapien
19	27	100.0	259	5	Q9VOT0		Q9VOT0 drosophila

ALIGNMENTS

RESULT 1
005422 PRELIMINARY;
ID 005422 PRT;
AC 005422; 38 AA.
DT 01-JUL-1997 (TREMBL); 04, Created
DT 01-JUL-1997 (TREMBL); 04, Last sequence update
DT 01-NOV-1998 (TREMBL); 08, Last annotation update
DE PHENYLENE DEHYDROGENASE (FRAGMENT).
DE CPTI.
GN OS
RA Mycobacterium marinum.
RC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN NCBI_TaxID=1781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M;
RX MEDLINE=7440138; PubMed=9294446;
RA Ramakrishnan L., Tran H.T., Federspiel N.A., Falkow S.;
RT "A crtB homolog essential for photochromogenicity in Mycobacterium
maximum: isolation, characterization, and gene disruption via
RT homologous recombination";
RL J. Bacteriol. 179:5862-5868 (1997).
DR U92075; AAB71427; 1.
FT NON_TER 1 1
SQ SEQUENCE 38 AA; 3985 MW; 6E46332707CCDCAB CRC64;

Query Match Score 27; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVGVP 5
1 1111
Db 3 GVGVP 7

RESULT 2
09REY0 PRELIMINARY;
ID 09REY0 PRT;
AC 09REY0; 88 AA.
DT 01-MAY-2000 (TREMBL); 13, Created
DT 01-MAY-2000 (TREMBL); 13, Last sequence update

DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)	OS	Ascovirus DPAV4.
DE	Renibacterium salmoninarum.	OC	Viruses; dsDNA viruses, no RNA stage; Ascoviridae; Ascovirus.
OS	Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Micrococccaceae; Micrococcineae; Micrococcaceae; Renibacterium.	OC	NCBI_TAXID=113365;
OC	Actinomycetales; Micrococccaceae; Micrococcineae.	OX	RN [1]
OX	NCBI_TAXID=1646;	RA	SEQUENCE FROM N.A.
RN	[1]	RA	MEDLINE=20540044; PubMed=11086137;
RP	SEQUENCE FROM N.A.	RA	Stasik K., Demattei M.V., Federici B.A., Bigot Y.;
RC	STRAIN=ATCC33209;	RT	"Phylogenetic position of the <i>Diadromus pulchellus</i> ascovirus DNA polymerase among viruses with large double-stranded DNA genomes.";
RA	Rhodes L.D., Strom M.S.;	RL	J. Gen. Virol. 81:1059-1072 (2000).
RT	"First insertion sequence identified in the salmon pathogen, <i>Renibacterium salmoninarum</i> ";	DR	EMBL; AR79812; CAC19116.1; -.
RT	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.	KW	Hypothetical protein.
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.	SQ	SEQUENCE 95 AA; 10441 MW; 14D90613A58F944A CRC64;
KW	Hypothetical protein.		
SQ	SEQUENCE 88 AA; 9971 MW; 495F4BFEE8B11FB3 CRC64;		
Query Match	Score 27; DB 2; Length 88; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match	Score 27; DB 14; Length 95; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GVGVGP 5	Qy	1 GVGVGP 5
Db	9 GVGVGP 13	Db	74 GVGVGP 78
RESULT	5	RESULT	5
Q9ZJ16	PRELIMINARY;	Q9ZJ16	PRELIMINARY;
ID	Q9ZJ16	ID	Q9ZJ16
AC	Q9ZJ16;	AC	Q9ZJ16;
Q9R322	PRELIMINARY;	PRT;	153 AA.
ID	Q9R322;	PRT;	88 AA.
AC	Q9R322;	PRT;	88 AA.
Q9R322;	PRELIMINARY;	PRT;	88 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)	DT	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DE	ICELAI.
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	GN	ICELAI.
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	OS	Helicobacter pylori (Campylobacter pylori)
DE	HYPOTHETICAL 9.9 kDa PROTEIN.	OC	Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OS	Renibacterium salmoninarum.	OC	Bacterium; Helicobacter.
OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Micrococccaceae; Micrococcineae; Micrococcaceae; Renibacterium.	OX	NCBI_TAXID=210;
OX	NCBI_TAXID=1646;	RN	[1]
RN	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RP	STRAIN=ATCC33209;	RC	STRAIN=ALASKA STRAIN 214;
RC	Rhodes L.D., Strom M.S.;	RA	Rauzonikiene A., Berg D.E.;
RA	"First insertion sequence identified in the salmon pathogen, <i>Renibacterium salmoninarum</i> ";	RT	"icelai gene from <i>H. pylori</i> (Alaska strain 214)" ;
RT	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.	RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.	DR	EMBL; AF001538; AAC64496.1; -.
DR	EMBL; AF163694; AF22735.1;	DR	InterPro; IPR03615;
DR	EMBL; AF163688; AF22723.1;	DR	SMART; SM00507; HHNC;
DR	EMBL; AF163689; AF22735.1;	DR	SEQUENCE 153 AA; 17347 MW; 38DE206C4B20B4E3 CRC64;
DR	EMBL; AF163690; AF22727.1;	Qy	1 GVGVGP 5
DR	EMBL; AF163692; AF22731.1;	Db	38 GVGVGP 42
DR	EMBL; AF163693; AF22733.1;		
KW	Hypothetical protein.		
SQ	SEQUENCE 88 AA; 9941 MW; B95F5AFEE8B11FAE CRC64;		
Query Match	Score 27; DB 2; Length 88; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match	Score 27; DB 2; Length 153; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GVGVGP 5	Qy	1 GVGVGP 5
Db	9 GVGVGP 13	Db	11111
RESULT	6	RESULT	6
Q9DSW9	PRELIMINARY;	Q9DSW9	PRELIMINARY;
ID	Q9DSW9;	ID	Q64778;
AC	Q9DSW9;	AC	Q64778;
Q9DSW9;	PRELIMINARY;	PRT;	161 AA.
ID	Q9DSW9;	PRT;	95 AA.
AC	Q9DSW9;	PRT;	95 AA.
Q9DSW9	PRELIMINARY;	PRT;	95 AA.
DT	01-MAR-2001 (TREMBLrel. 16, Created)	DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	DT	01-MAR-2001 (TREMBLrel. 01, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	DE	DNA FRAGMENT.
DE	Avian adenovirus gall (strain Phelps) (Fowl adenovirus 1) (CELO).	OS	Avian adenovirus gall (strain Phelps) (Fowl adenovirus 1) (CELO).
OC	Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenvirus.	OC	Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenvirus.
NCBI_TAXID=1053;	OX	NCBI_TAXID=1053;	OX
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAIN=CELO;	RC	AKOPIAN T.A., Kaverina E.N., Kruglyak V.A., Naroditsky B.S.,
RA			

RA Tikhonenko T.T.;
 RL Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; 222866; CAA80482.1; -;
 SQ SEQUENCE 161 AA; 17871 MW; DDA8934B88C1BF6 CRC64;

Query Match Score 27; DB 14; Length 161;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GVGVP 5
 Db 57 GVGVP 61

RESULT 7
 P78931 PRELIMINARY; PRT; 178 AA.
 ID P78931; AC P78931; DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-MAY-1997 (TREMBLrel. 03, Last annotation update)
 DE FISSION YEAST DNA FOR ISPA4, PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, ATFL,
 DB CHROMOSOME II COSMID 1228 SEQUENCE.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryote; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TAXID=4896;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=N2H;
 RA Kohno A., Niwa O., Yano M., Saitoh S., Katayama T., Nagao K.,
 RA Yanagida M.;
 RT "S.pombe chromosome II cosmid 1228 sequence."
 RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
 DR D83952; BAA12179.1; -;
 SQ SEQUENCE 178 AA; 20631 MW; 57ECB30E2E4CF656 CRC64;

Query Match Score 27; DB 3; Length 178;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GVGVP 5
 Db 5 GVGVP 9

RESULT 8
 056970 PRELIMINARY; PRT; 206 AA.
 ID 056970; AC 056970; DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DB 21.7 KDA PROTEIN
 OS Maize streak virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 OX NCBI_TAXID=10821;
 RN [1]
 SEQUENCE FROM N.A.
 RC Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 RN [2]

RL Arch. Virol. 141:1637-1650(1996);
 DR EMBL; AJ224568; CAA12004.1; -;
 SQ SEQUENCE 206 AA; 21743 MW; 553E4A41A9EEF3AF4 CRC64;

Query Match Score 27; DB 14; Length 206;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GVGVP 5
 Db 128 GVGVP 132

RESULT 9
 073468 PRELIMINARY; PRT; 206 AA.
 ID 073468; AC 073468; DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE 21.7 KDA PROTEIN.
 OS Maize streak virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 OX NCBI_TAXID=10821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2A;
 RX MEDLINE=97049057; PubMed=8893787;
 RA Peterschmitt M., Granier M., Frutos R., Reynaud B.;
 RT "Infectivity and complete nucleotide sequence of the genome of a
 genetically distinct strain of maize streak virus from Reunion
 Island.";
 RT Arch. Virol. 141:1637-1650(1996).
 RN [2]

Query Match Score 27; DB 14; Length 206;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GVGVP 5
 Db 128 GVGVP 132

RESULT 10
 073472 PRELIMINARY; PRT; 206 AA.
 ID 073472; AC 073472; DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE 21.7 KDA PROTEIN.
 OS Maize streak virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 OX NCBI_TAXID=10821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2A;
 RX MEDLINE=97049057; PubMed=8893787;
 RA Peterschmitt M., Granier M., Frutos R., Reynaud B.;
 RT "Infectivity and complete nucleotide sequence of the genome of a
 genetically distinct strain of maize streak virus from Reunion
 Island.";
 RT Arch. Virol. 141:1637-1650(1996).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=SP1;
 RA Isnard M., Granier M., Frutos R., Reynaud B.; Peterschmitt M.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ225007; CAA12310.1;
 SQ SEQUENCE 206 AA; 21842 MW; 488897FLB3459BE1 CRC64;

Query Match Score 27; DB 14; Length 206;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DE 21.7 KDA PROTEIN.

QY 1 GVGVGP 5
 Db 128 GVGVGP 132
 SQ SEQUENCE 206 AA; 21743 MW; 488897FLA9EEF3AF0 CRC64;

RESULT 11
 ID O73474 PRELIMINARY; PRT; 206 AA.
 AC O73474;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-NOV-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE 21.7 KDA PROTEIN.
 OS Maize streak virus.
 OX Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 NCBI_TaxID=10821;
 RN SPAIN-SP2;
 RP SEQUENCE FROM N.A.
 RC STRAIN=SP2;
 RX MEDLINE=97040507; PubMed=8893787;
 RA Peterschmitt M., Granier M., Frutos R., Reynaud B.;
 RT "Infectivity and complete nucleotide sequence of the genome of a
 genetically distinct strain of maize streak virus from Reunion
 Island.";
 RT Arch. Virol. 141:1637-1650(1996).
 RN SEQUENCE FROM N.A.
 RC SPAIN-SP2;
 RA Isnard M., Granier M., Frutos R., Reynaud B.; Peterschmitt M.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ225008; CAA12317.1;
 SQ SEQUENCE 206 AA; 21726 MW; 428987FLB8EE2646 CRC64;

Query Match Score 27; DB 14; Length 206;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DE 21.7 KDA PROTEIN.

QY 1 GVGVGP 5
 Db 128 GVGVGP 132
 SQ SEQUENCE 206 AA; 21743 MW; 488897FLA9EEF3AF0 CRC64;

RESULT 12
 ID Q83476 PRELIMINARY; PRT; 206 AA.
 AC Q83476;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 21.7 KDA PROTEIN.
 OS Maize streak virus.
 OX Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 NCBI_TaxID=10821;
 RN SEQUENCE FROM N.A.
 RA Isnard M., Granier M., Frutos R., Reynaud B.; Peterschmitt M.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN SPAIN-SP2;
 RP MEDLINE=97040507; PubMed=8893787;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 Coulson A., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 Jones M., Kershaw J., Laird N., Latrellie P.,
 Lightning J., Lloyd C., McMurray A., Mortimer B., O'Callaghan M.,
 Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Shownkeen R.,
 Smalldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
 Terrierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 Watson A., Weinstock L., Wilkinson-Spratt J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL; 233236; CAB05780.1;
 SQ SEQUENCE 214 AA; 23253 MW; EEE0E593A7D625560 CRC64;

Query Match Score 27; DB 5; Length 214;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVGVGP 5
 Db 195 GVGVGP 199
 SQ SEQUENCE FROM N.A.
 RA Isnard M., Granier M., Frutos R., Reynaud B.; Peterschmitt M.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN SPAIN-SP2;
 RP MEDLINE=97040507; PubMed=8893787;

ID	Q9KYY0;	PRELIMINARY;	PRT;	223 AA.			
AC	Q9KYY0;						
DR	01-OCT-2000 (TREMBLrel. 15, Created)						
DT	01-MAR-2001 (TREMBLrel. 15, Last sequence update)						
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)						
DE	PUTATIVE PHOSPHATASE.						
GN	SCE33_002C.						
OS	Streptomyces coelicolor.						
OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;						
OC	Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.						
OX	NCBI_TAXID=1902;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=A3(2);						
RA	Saunders D.C., Harris D.;						
RL	Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=A3(2);						
RX	MEDLINE=97000351; PubMed=8843436;						
RA	Redenbach M., Kleiser H.M., Denaparte D., Eichner A., Cullum J.,						
RA	Kinashii H., Hopwood D.A.;						
RT	"A set of ordered cosmids and a detailed genetic and physical map for						
RT	the 8 Mb Streptomyces coelicolor A3(2) chromosome."						
RL	Mol. Microbiol. 21:77-96(1996).						
DR	EMBL: AL355774; CAB90911.1; -						
DR	InterPro: IPR001454; -						
DR	pfam: PF00702; Hydrolase_1;						
SQ	SEQUENCE 223 AA; 23869 MW; 1D14700B7DA9B241 CRC64;						
Query Match	Best Local Similarity 100.0%	Score 27;	DB 2;	Length 223;			
Matches	5; Conservative 100.0%	Pred. No. 4.7e+02;					
		Mismatches 0;	Indels 0;	Gaps 0;			
Qy	1 GVGVP 5						
Db	202 GVGVP 206						
RESULT	15						
Q9DDR8	Q9DDR8 PRELIMINARY;	PRT;	240 AA.				
ID	Q9DDR8;						
AC	Q9DDR8;						
DT	01-MAR-2001 (TREMBLrel. 16, Created)						
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)						
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)						
DE	NA/PI COTRANSPORTER NAPI-IIA (FRAGMENT).						
OS	Gallus gallus (Chicken).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;						
OC	Gallus.						
OX	NCBI_TAXID=9031;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE KIDNEY;						
RA	Werner A., Kinne R.K.H. Jr.;						
RT	"The evolution of the Na+/Pi cotransport systems."						
RT	Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.						
RL	EMBL: AF29188; AAG3802.1; -						
FT	NON_TER 1						
FT	NON_TER 240 240 AA;						
SQ	SEQUENCE 240 AA; 25214 MW; F02283AAC242496C CRC64;						
Query Match	Best Local Similarity 100.0%	Score 27;	DB 13;	Length 240;			
Matches	5; Conservative 100.0%	Pred. No. 5.1e+02;	Mismatches 0;	Indels 0;	Gaps 0;		

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OM protein - protein search, using sw model

Run on: July 25, 2001, 16:49:30 ; Search time 32.96 seconds
(without alignments)
9.197 Million cell updates/sec

Title: US-09-251-638-2
Perfect score: 27
Sequence: 1 GvGVP 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.0%
Maximum Match 1.00%
Listing First 45 summaries

Database : A_Geneseq_0601-*

1: /SIDS8/gcadata/geneseq/geneseq/AA1980.DAT;*: 1
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12: /SIDS8/gcadata/geneseq/geneseq/AA1991.DAT;*: 1
13: /SIDS8/gcadata/geneseq/geneseq/AA1992.DAT;*: 1
14: /SIDS8/gcadata/geneseq/geneseq/AA1993.DAT;*: 1
15: /SIDS8/gcadata/geneseq/geneseq/AA1994.DAT;*: 1
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18: /SIDS8/gcadata/geneseq/geneseq/AA1997.DAT;*: 1
19: /SIDS8/gcadata/geneseq/geneseq/AA1998.DAT;*: 1
20: /SIDS8/gcadata/geneseq/geneseq/AA1999.DAT;*: 1
21: /SIDS8/gcadata/geneseq/geneseq/AA2000.DAT;*: 1
22: /SIDS8/gcadata/geneseq/geneseq/AA2001.DAT;*: 1

RESULT 1
ID AAR04173
XX standard; protein; 5 AA.
AC AAR04173;
XX DT 10-SEP-1990 (first entry)
XX DE Monomer of repetitive primary structure of a synthetic fibrous protein.
XX KW Collagen; elastin; keratin; tropoerin C; silk; dopa protein; synthetic skin; cosmetics; bioadhesive.
XX OS Synthetic.
XX PN WO0003438-A.
XX PD 05-APR-1990.
XX PR 06-SEP-1989; 89WO-0003839.
XX PR 30-SEP-1988; 88US-0251714.
XX PA (ALLIANCE) ALLIED SIGNAL INC.
XX PI Goldberg I, Salerno AJ;
XX DR WPI; 1990-132274/17.
XX PT New bacterial strains for heterologous gene expression -
PT contg. elements for initiating activity, retarding proteolysis
PT and stabilising heterologous genes.
XX

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	1 AAR04173	Nonamer of repeat
2	27	100.0	5	16 AAR65230	Fibrinogen/beta-c
3	27	100.0	5	17 AAW01440	Beta turn peptide
4	27	100.0	5	17 AAW09207	Elastin repeat pep
5	27	100.0	5	18 AAW22711	Bioelastomeric rep
6	27	100.0	5	18 AAW26331	Elastin repeat uni
7	27	100.0	5	18 AAW18263	Transglutaminase C
8	27	100.0	5	19 AAW53505	peptide repeat un
9	27	100.0	5	20 AAY31689	Pentapeptide used
10	27	100.0	5	20 AAY04125	Protein based poly
11	27	100.0	5	21 AAY51876	Elastin peptide re

PS	Disclosure; ; 1pp; English.	Matches	5	Conservative	0	Mismatches	0	Indels	0	Gaps	0;	
XX	The polymer of the peptide may act as an analogue to peptides containing a repetitive or quasi-repetitive structure e.g. collagen, elastin, keratin, tropoelastin, C, dopa proteins, silk proteins, biodegradable proteins and insect cuticle Proteins. These products may be useful in the manufacture of fibrous products, synthetic skin and cosmetic additives.	Qy	1 GVGVP 5 1 gvgvp 5	AC	AAW01440	ID	AAW01440 standard; peptide; 5 AA.	XX				
CC		AC	AAW01440;	XX								
CC		DR	18-JUN-1997 (first entry)	XX								
CC		DE	Beta turn peptide GVGVP.	XX								
CC		KW	Beta turn; artificial Polymer; inverse temperature transition; bioelastomer; repeat unit.	XX								
CC		RESULT	3	OS								
CC		XX	AAW01440	OS								
CC	Sequence 5 AA;	XX		Synthetic.								
CC		XX	W09632406-A1.	XX								
CC		XX		PD	17-OCT-1996.							
CC		XX		PP	15-APR-1996;	96WO-US05186.						
CC		XX		PR	13-OCT-1995;	95US-0543020.						
CC		XX		PR	14-APR-1995;	95US-0423516.						
CC		XX		PA	(BIOE-) BIOELASTICS RES LTD.							
CC		XX		PA	(UABR-) UAB RES FOUND.							
CC		XX		PI	Mcpherson DT, Urry DW, xu J;							
CC		XX		DR	WPI; 1996-477065/47.							
CC		XX		PP	Purifying artificial polymer exhibiting reversible inverse temp.							
CC		XX		PT	transition - specifically bioelastic polymers from complex mixtures							
CC		XX		PT	of proteins, e.g., those found after expression in host.							
CC		XX		PS	Example 1; Page 27; 46pp; English.							
CC		XX		XX	This sequence represents a beta turn peptide. This sequence was used as a repeating unit in an artificial polymer, which exhibits reversible inverse temperature transition, purified by the method of the invention.							
CC		XX		CC	The method of the invention comprises dissolving the polymer in an aqueous medium and adjusting the relative temperature of the aqueous medium to the effective transition temperature of the polymer, so that the temperature of the aqueous medium is below the effective transition temperature. Any particulate material present in the medium is then removed, and the relative temperature of the aqueous medium is adjusted to the effective transition temperature of the polymer, so that the temperature of the aqueous medium is above the effective transition temperature of the polymer. Dense phase material comprising the polymer is then collected from the medium until a desired level of purity is reached. The method is used for the purification of polymers that exhibit inverse temperature transition to a high degree of purity for their commercial application, specifically bioelastomers irrespective of their source. The method is particularly advantageous for purifying bioelastomeric polypeptides from complex mixtures of proteins, e.g., those found after expression of bioelastomer.c							
CC		XX		CC	polypeptides in a host, and can also be used to purify chemically synthesised peptides.							
CC		XX		CC	Sequence 5 AA;							
CC		XX		Query Match	100.0%	Score 27; DB 17;	Length 5;					
CC		XX		Best Local Similarity	100.0%	Pred. No. 3.4e+05;						
CC		XX		Matches	5	Mismatches 0;	Indels 0;	Gaps 0;				

QY 1 GVGYP 5
DB 1 gvgvp 5

RESULT 4
AAW09207 standard; peptide: 5 AA.
ID AAW09207
XX
AC AAW09207
DT 29-MAR-1997 (first entry)
XX
DE Elastin repeat peptide.
XX
KW Elastin; repeat unit; protein polymer; crosslinking; adhesive; tissue sealant; biocompatible film.
XX
OS Synthetic.
XX
PN WO9634618-A1.
XX
PD 07-NOV-1996.
XX
PF 02-MAY-1996; 96WO-US062229.
XX
PR 05-MAY-1995; 95US-0435641.
XX
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX
PI Cappelio J, Stedronsky ER,
XX
DR WPI: 1996-505895/50.

Tissue repair adhesive comprising polymer of structural protein repeat units - contng. hetero-atom functional gags reactive with crosslinking agent, combines biocompatibility and high bonding strength.

Claim 4: Page 96; 101PP; English.

This peptide is a repeat unit derived from elastin, and may be used in construction of a protein polymer backbone, which may be crosslinked chemically to form a strongly adherent tissue adhesive or sealant. The polymer may be incubated with a polyfunctional crosslinking agent to form the adhesive. The repeat unit may be used with silk fibroin peptide AAW09206 at a ratio of 1:16:1 to form a block copolymer protein, e.g. AAW09213, AAW09218, AAW09219, AAW09223. At least one of the repeats may be modified to introduce a crosslinking functionality. The polymer may be used to seal defects in vessel walls, e.g. artery, vein, capillary, lung, dura or colon, to increase tissue mass, or to produce biocompatible films for in vivo use. The sealants have the biocompatibility of fibrin glues, but set more quickly, and have greater strength. They are readily prepared by recombinant methods, are easy to administer, and are gradually resorbed.

XX Sequence 5 AA;

AC AAW22711;
XX DT 26-FEB-1998 (first entry)
XX DE Bioelastomeric repeating unit 4 responsive to electrical energy.
XX KW Bioelastomeric repeating unit; polymer; inverse temperature transition; electrical energy change; polarity; hydrophobicity; mechanical work; surgical suture; heat shrinkable membrane; desalination.
XX OS Synthetic.
XX PN WO9723729-A1.
XX PD 03-JUL-1997.
XX PF 07-JUN-1996; 96WO-US09776.
XX PR 07-JUN-1995; 95US-0487594.
XX PA (URRY/) URRY D W.
XX PI URRY DW;
XX DR WPI: 1997-363360/33.
XX PT Bioelastomeric polymer responsive to electrical energy - comprising beta turn and residue(s) with side chain that changes polarity or hydrophobicity in response to electrical energy change, useful for mechanical work or light stimulated contraction.
XX Example 1: Page 47; 60pp; English.
XX AAW22711-16 represent bioelastomeric repeating units that are used to create a polymer responsive to electrical energy. This bioelastomeric polymer comprises a bioelastomeric polypeptide having an inverse temperature transition, and a repeating bioelastomeric unit containing at least 1 beta-turn and residues with a side chain. The side chain of these residues responds to an electrical energy change by altering its polarity or hydrophobicity. The side chain is present in sufficient amounts to provide a shift in the inverse temperature transition of the polymer upon the change in exposure to electrical energy. The polymer may also contain a second amino acid with a side chain capable of undergoing a change in an aqueous environment. The polymers (AAW34881-83) consist of the formulas described in AAW22716 and AAW22714 and below:
CC poly[0.57(GVGYP), 0.33(GFGVP), 0.1(GKGVYP)]
CC The expansion or contraction of the polymer upon exposure to a change in electrical energy can be used to produce mechanical work when the polymer is constrained. It can also cause turbidity and chemical changes in a closed environment. The polymer can be used in surgical sutures, especially for microsurgery, heat shrinkable membranes, controlled herbicide or pesticide release or for desalination.
XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVGYP 5
DB 1 gvgvp 5

RESULT 5
AAW22711 standard; Peptide; 5 AA.
ID AAW26331;
XX AC AAW26331;
XX DT 19-NOV-1997 (first entry)
XX

XX Preparation of synthetic repetitive DNA - useful for construction of
PT large protein polymers having repeating units, used in structural
PR material, e.g. synthetic silk
XX Claim 11; Page 22; 127PP; English.
PS This is the amino acid sequence of the peptide repeat unit, used in the
XX method of the invention, which involves the preparation of synthetic
CC DNA sequence having repeating units from about 3-15 codons and encoding
CC a protein of at least about 30 kDa. The method is useful for the
CC production of high molecular weight polymers (e.g. synthetic silk),
CC either nucleic acids or peptides that are the expression products of
CC the nucleic acids and particularly high molecular weight peptides
CC containing repeating units which are useful as structural materials.
XX Sequence 5 AA:

Query	Match	Score	DB	Length	5;	
Best	Local	Similarity	No.	Mismatches	Indels	Gaps
Qy	1	GGVGP	5		0;	0;
Db	1					
		gvgvp	5			

RESULT 9

AY31689

AY31689 standard; Peptide; 5 AA.

XX

AC

AY31689;

XX

DT

22-NOV-1999 (first entry)

XX

DE

X

DE

XX

KW

Elastomer; bioelastomer; polymer; tissue augmentation; elastin;

KW

tissue restoration; tissue reconstruction; tissue repair; implant.

OS

Synthetic.

XX

W0943271-A1.

XX

PD

02-SEP-1999.

XX

PF

26-FEB-1999;

99WO-US04440.

XX

PR

29-MAY-1998;

98US-008715.

PR

27-FEB-1998;

98US-0072297.

XX

PA (BIOE-) BIOELASTICS RES LTD.

XX

Glazer PA,

Parker TM,

Urry DW;

XX

WPI: 1999-540487/45.

XX

Augmentation or restoration of mammalian tissue by injecting

PT solution of peptide polymer, used for soft or hard tissue

reconstruction, especially of intervertebral disks

PS

Claim 9; Page 81; 133PP; English.

XX The present sequence represents an example of a pentapeptide that
PT is used in novel bioelastic polymers. The invention provides a
PR method of tissue augmentation by injecting a polymer comprising
PS repeating peptide monomeric units selected from nonapeptide,
XX pentapeptide and tripeptide monomeric units, where the monomeric
XX units form a series of beta-turns separated by dynamic bridging
XX segments. The Polymer has an inverse temperature transition value
CC that is less than the tissue temp and is injected in water
CC solution at coacervate concentration. The polymer can be injected
CC

CC at periurethral or subdermal sites (for treatment of urinary
CC incontinence or for cosmetic purposes), or into hard or soft
CC tissue, e.g. for repair of traumatic injury. A specific
CC application is restoration of intervertebral discs. The elastin
CC type polymer based on the present pentapeptide, when prepared with
CC repeat units in the order of 200 and when cross-linked, provides an elastic modulus
CC gamma-irradiation, forms an elastic matrix with an elastic capacity
CC approximating that of the vascular wall, providing the capacity
CC to match compliance over a wide range of biological tissues.

Query	Match	Score	DB	Length	5;	
Best	Local	Similarity	No.	Mismatches	Indels	Gaps
Qy	1	GVGVP	5		0;	0;
Db	1					
		gvgvp	5			

RESULT 10

AY04125

AY04125 standard; peptide; 5 AA.

XX

AC

AY04125;

XX

DT

11-JUN-1999 (first entry)

XX

DE

Protein based polymer pentamer peptide sequence.

XX

Kw

Chloroplast integration; expression vector; transformation; PBP;

XX

Kw

protein based polymer; herbicide resistance.

OS

Synthetic.

XX

PN

WO910513-A1.

XX

PD

04-MAR-1999.

XX

PF

05-AUG-1998;

98WO-TB01199.

XX

PR

15-MAY-1998;

98US-0079640.

PR

07-AUG-1997;

97US-0055314.

PR

23-MAR-1998;

98US-0079042.

XX

PA (UYAU-) UNIV AUBURN.

XX

PI

Daniell H;

XX

DR

WPI; 1999-190626/16.

XX

New universal chloroplast integration and expression vectors -

PT

The present invention describes a novel universal integration and

CC

expression vector (A) competent for stably transforming the chloroplast

CC

genome of different plant species. Products from the present invention

CC

can be used for producing transformed plants such as maize, rice, grass,

CC

rye, barley, oat, wheat, soybean, peanut, grape, sweet potato, pea,

CC

canola, tobacco, tomato or cotton. The transformed plants can be used

CC

for producing polypeptides of interest, e.g. insulin or human serum

CC

albumin. The plants can also be made resistant to herbicides e.g.

CC

glycophosates, paraquat, atrazine, dinoseb, lenacil, mebribazine,

CC

cyclohexanone, haloxyfop, clethodim and phenoxaprop, MCPA, 2,4-D,

CC

dinotefuran, sulfonylureas, imidazolinones, bromoxynil, methyl sulfonyl,

CC

chlorotoluron, phosphinothricin or imazapyr. They can also be made

CC

resistant to insects e.g. tobacco budworm, cottonboll worm or beet

CC

PS Disclosure: Page 51; 137pp; English.

xx The invention relates to biomolecules comprising elastomeric peptides.
cc The elastomeric peptide contracts in response to a change in some
cc environmental parameter. The properties of the functional components in
cc the biomolecule are altered when contraction or expansion of the
cc elastomeric peptides is induced. The biomolecules are used: (i) for
cc purification, based on affinity of its functional component, as an
cc antibody, and its ability to release bound material after induction of
cc expansion or contraction; (ii) as a pharmaceutical, for extracorporeal
cc treatment or localized systemic treatment, e.g. by exploiting variations
cc in pH in the digestive tract or of temperature at sites of infection;
cc (iii) as a biosensor to detect changes in the environment of the
cc molecule, e.g. activation of an enzyme to generate a coloured product,
cc also in enzyme-linked immunosorbent and other assays, for screening
cc expression libraries by panning and generally for diagnosis; or (iv)
cc where the functional component is an enzyme, as reagent for e.g. PCR
(polymerase chain reaction), e.g. a polymerase that becomes active only
cc at a selected temperature, in fermentations, etc. The elastomeric peptide
cc provides an inducible switch which may eliminate, increase or reduce
cc activity; alter activity, e.g. change the kinetic parameters for a
cc particular enzymatic or binding reaction, or introduce new activity,
cc especially for control of enzymatic activity, e.g. in PCR as an
cc alternative to the 'hot start' technique.
xx

SQ Sequence 8 AA;

Query Match 100.0%; Score 27; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVGVP 5
Db 1 gvgvp 5

Search completed: July 25, 2001, 16:49:31
Job time: 43 sec

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OM protein - protein search, using sw model

Run on: July 25, 2001, 16:49:56 ; Search time 20.09 Seconds
(without alignments)

5.125 Million cell updates/sec

Title: US-09-251-638-2

Perfect score: 27

Sequence: 1 GvGVP 5

Scoring table: BLOSH62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Description	
Result No.	Score	Query	Match	Length	DB ID
1	27	100.0	5	1	US-09-106-509-14
2	27	100.0	5	1	US-09-175-155-3
3	27	100.0	5	1	US-08-477-509B-23
4	27	100.0	5	2	US-08-435-641-2
5	27	100.0	5	2	US-08-707-237A-9
6	27	100.0	5	2	US-08-543-020-1
7	27	100.0	5	2	US-08-483-236-17
8	27	100.0	5	2	US-08-735-692-3
9	27	100.0	5	3	US-08-542-051-41
10	27	100.0	5	3	US-08-482-085B-23
11	27	100.0	5	3	US-08-642-246-2
12	27	100.0	5	3	PCT-US96-06229-2
13	27	100.0	5	6	5250516-16
14	27	100.0	7	3	US-09-039-308A-40
15	27	100.0	15	2	US-08-735-692-15
16	27	100.0	16	1	US-08-468-543-17
17	27	100.0	16	2	US-08-469-692-17
18	27	100.0	16	2	US-08-398-046-17
19	27	100.0	20	1	US-08-127-351-35
20	27	100.0	20	1	US-08-480-367B-35
21	27	100.0	20	1	US-08-487-221A-35
22	27	100.0	20	1	US-08-480-370-35
23	27	100.0	20	1	US-08-299-636-14
24	27	100.0	20	1	US-08-279-155-16
25	27	100.0	20	1	US-08-464-456-14
26	27	100.0	20	1	US-08-486-135-2
27	27	100.0	20	1	US-08-703-988A-16

ALIGNMENTS

RESULT 1
US-08-106-509-14
; Sequence 14, Application US/08106509
; Patent No. 5428014

; GENERAL INFORMATION:
; APPLICANT: Labroo, Virender
; TITLE OF INVENTION: TRANSGLUTAMINASE CROSS-LINKABLE
; TITLE OF INVENTION: POLYPEPTIDES AND METHODS RELATING THERETO
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105

; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/106,509
FILING DATE: 19930813
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-106-509-14

Query Match 100.0%; Score 27; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
Db 1 GVGVP 5

RESULT 2

US-08-175-155-3

; Sequence 3, Application US/08175155

; Patent No. 5641648

; GENERAL INFORMATION

; APPLICANT: Ferrari, Franco A.

; APPLICANT: Cappello, Joseph W.

; APPLICANT: Crissman, John W.

; APPLICANT: Dormai, Mary A.

; TITLE OF INVENTION: Methods for Preparing Synthetic

; TITLE OF INVENTION: Repetitive DNA

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flier, Hohbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477-509B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/175,155

FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/053,049

FILING DATE: 22-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986

ATTORNEY/AGENT INFORMATION:

NAME: Trecatin, Richard F.

REGISTRATION NUMBER: 31,801

REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1889

TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: Linear

MOLECULE TYPE: peptide

US-08-477-509B-23

Query Match 100.0%; Score 27; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.5e+05;

Matches 5; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

US-08-435-641-2

; Sequence 2, Application US/08435641

; Patent No. 5817303

; GENERAL INFORMATION

; APPLICANT: Sedrinsky, Erwin R.

; TITLE OF INVENTION: Tissue Adhesive Using Synthetic

; TITLE OF INVENTION: Crosslinking

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/435,641

FILING DATE: 05-MAY-1995

RESULT 3

US-08-477-509B-23

; Sequence 23, Application US/08477509B

; Patent No. 5770697

; GENERAL INFORMATION

; APPLICANT: Ferrari, Franco A.

; APPLICANT: Cappello, Joseph W.

; APPLICANT: Crissman, John W.

; APPLICANT: Dormai, Mary A.

; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive

; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same

; NUMBER OF SEQUENCES: 112

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flier, Hohbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertram I.
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: A-61127
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEX: 415-781-3249
 TELEFAX: 415-781-3249
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-435-641-2

Query Match Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 GVGV P 5
 |||||
 Db 1 GVGV P 5

RESULT 5

US-08-707-237A-9

Sequence 9, Application US/08707237A
 Patent No. 5830713

GENERAL INFORMATION:

ATTORNEY: Ferrari, Franco A.

APPLICANT: Capello, Joseph

APPLICANT: Crisman, John W.

APPLICANT: Dorman, Mary A.

TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC

TITLE OF INVENTION: REPETITIVE DNA

NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fiehr, Hohbaeh, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/707,237A

FILING DATE: 03-SEP-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/175,155

FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/053,049

FILING DATE: 22-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/609,716

FILING DATE: 06-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/269,429

FILING DATE: 09-NOV-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987

APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986

ATTORNEY/AGENT INFORMATION:
 NAME: Trecartin, Richard F.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-55186-10/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 27729
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-707-237A-9

Query Match Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 GVGVP 5
 |||||
 Db 1 GVGVP 5

RESULT 6

US-08-543-020-1

Sequence 1, Application US/08543020

Patent No. 5854387

GENERAL INFORMATION:

ATTORNEY: Urry, Dan W.

APPLICANT: McPherson, David T.

APPLICANT: Xu, Jie

TITLE OF INVENTION: A Simple Method for the Purification of

TITLE OF INVENTION: a Bioelastic Polymer

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

STREET: 5 Palo Alto Square

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94306-2155

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/543,020

FILING DATE: 13-OCT-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Hughes, Melya J.

REGISTRATION NUMBER: 38,696

REFERENCE/DOCKET NUMBER: BERL-016/010S

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415 853 5070

TELEFAX: 415 857 0663

TELEX: 380816COOLEYPA

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

TOPOLOGY: Linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-543-020-1

Query Match 100.0%; Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGV P
 Db 1 GVGV P

RESULT 7
 US-08-483-236-17
 ; Sequence 17, Application US/08483236
 ; Patent No. 5939385
 ; GENERAL INFORMATION:
 ; APPLICANT: Labroo, Virender
 ; APPLICANT: Busby, Sharon
 ; TITLE OF INVENTION: Transglutaminase Cross-Linkable
 ; TITLE OF INVENTION: Polypeptides and Methods Relating Thereto
 ; NUMBER OF SEQUENCES: 18
 ; NUMBER OF SEQUENCES: 18
 ; ADDRESSEE: Symgenetics, Inc.
 ; STREET: 1201 Eastlake Avenue East
 ; CITY: Seattle
 ; STATE: WA
 ; ZIP: 98102
 ; COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,236
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Parker, Gary E.
 REGISTRATION NUMBER: 31-648
 REFERENCE/DOCKET NUMBER: 93-09c1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6673
 TELEFAX: 206-442-6678
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-483-236-17

Query Match 100.0%; Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGV P
 Db 1 GVGV P

RESULT 8
 US-08-735-692-3
 ; Sequence 3, Application US/08735692B
 ; Patent No. 5972406
 ; GENERAL INFORMATION:
 ; APPLICANT: Ury, Dan W.
 ; APPLICANT: Prasad, Kari
 ; APPLICANT: Sherry, Peter R.
 ; TITLE OF INVENTION: Bielastomers Suitable as Food Product Additives
 ; CURRENT APPLICATION NUMBER: US/08/735,692B
 ; CURRENT FILING DATE: 1995-10-16

; EARLIER APPLICATION NUMBER: 08/423,517
 ; EARLIER FILING DATE: 1995-04-14
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 3
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:synthetic
 US-08-735-692-3

Query Match 100.0%; Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGV P
 Db 1 GVGV P

RESULT 9
 US-08-542-051-41
 ; Sequence 41, Application US/08542051F
 ; Patent No. 6004782
 ; GENERAL INFORMATION:
 ; APPLICANT: Daniel, Henry
 ; APPLICANT: McPherson, David T.
 ; APPLICANT: Ury, Dan W.
 ; APPLICANT: Xu, Jie
 ; TITLE OF INVENTION: Hyperexpression of Bicelastic Polypeptides
 ; FILE PREFERENCE: BERL-018/01US
 ; CURRENT APPLICATION NUMBER: US/08/512,051F
 ; CURRENT FILING DATE: 1995-10-13
 ; EARLIER APPLICATION NUMBER: 08/423,642
 ; EARLIER FILING DATE: 1995-04-14
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 41
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:synthetic
 US-08-542-051-41

Query Match 100.0%; Score 27; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGV P
 Db 1 GVGV P

RESULT 10
 US-08-482-085B-23
 ; Sequence 23, Application US/08482085B
 ; Patent No. 6018030
 ; GENERAL INFORMATION:
 ; APPLICANT: Ferrari, Franco A.
 ; APPLICANT: Richardson, Charles
 ; APPLICANT: Chambers, James
 ; APPLICANT: Causey, Stuart
 ; APPLICANT: Pollack, Thomas J.
 ; APPLICANT: Cappello, Joseph
 ; APPLICANT: Crissman, John W.
 ; TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive
 ; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
 ; NUMBER OF SEQUENCES: 112
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,085B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 06/927,258
 FILING DATE: 04-NOV-1986
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/114,618
 FILING DATE: 29-OCT-1987
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/053,049
 FILING DATE: 22-APR-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/175,155
 FILING DATE: 29-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Trecartin, Richard F.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-482-085B-23

Query Match 100.0%; Score 27; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
 Db 1 GVGVP 5

RESULT 11
 US-08-642-246-2

GENERAL INFORMATION:
 Patent No. 6033654
 Sequence No. Application US/08642246
 ATTORNEY: STEDRONSKY, Irwin R.
 APPLICANT: CAPPELLO, Joseph
 TITLE OF INVENTION: Tissue Adhesive Using Synthetic
 TITLE OF INVENTION: Crosslinking
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
 STREET: Four Embarcadero Center, Suite 200
 CITY: San Francisco
 STATE: CA
 COUNTRY: US
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/06229
 FILING DATE:

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: ROWLAND, Bertteam I
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: A61127-1/BIR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-642-246-2

Query Match 100.0%; Score 27; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
 Db 1 GVGVP 5

RESULT 12
 PCT-US96-06229-2

Sequence 2, Application PCT/US96/06229
 GENERAL INFORMATION:
 APPLICANT: STEDRONSKY, Irwin R.
 APPLICANT: CAPPELLO, Joseph R.
 TITLE OF INVENTION: Tissue Adhesive Using Synthetic
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
 STREET: Four Embarcadero Center, Suite 200
 CITY: San Francisco
 STATE: CA
 COUNTRY: US
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/06229
 FILING DATE:

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/06229
 FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: ROWLAND, Bertteam I
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: A61127-1/BIR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US96-06229-2

Query Match Best Local Similarity Score 27; DB 5; Length 5;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
 Db 1 GVGVP 5

RESULT 13
 5250516-16
 ; Patent No. 5250516
 ; APPLICANT: URRY, DAN W.
 ; TITLE OF INVENTION: BIOLASTOMERIC MATERIALS SUITABLE FOR
 ; THE PROTECTION OF BURN AREAS OR THE PROTECTION OF WOUND
 ; REPAIR SITES FROM THE OCCURRENCE OF ADHESIONS
 ; NUMBER OF SEQUENCES: 18
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/184,407
 ; FILING DATE: 21-APR-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 900,895
 ; FILING DATE: 27-AUG-1986
 ; APPLICATION NUMBER: 853,212
 ; FILING DATE: 17-APR-1986
 ; SEQ ID NO:16;
 ; LENGTH: 5

5250516-16
 Query Match Best Local Similarity Score 27; DB 6; Length 5;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
 Db 1 GVGVP 5

RESULT 14
 US-09-039-308A-40
 ; Sequence 40, Application US/09039308A
 ; GENERAL INFORMATION:
 ; APPLICANT: Sandberg, Lawrence; Roos, Phillip;
 ; TITLE OF INVENTION: MITTS, Thomas ELASTIN DERIVED COMPOSITION
 ; TITLE OF INVENTION: AND METHOD OF
 ; TITLE OF INVENTION: USING SAME
 ; NUMBER OF SEQUENCES: 41
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: REED SMITH SHAW & MCCLAY, LLP
 ; STREET: PO Box 488
 ; CITY: Pittsburgh
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 15230
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
 ; COMPUTER: Compaq
 ; OPERATING SYSTEM: Microsoft Windows 95
 ; SOFTWARE: Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/039, 308A
 ; FILING DATE: March 13, 1998
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Miller, Raymond A.
 ; REGISTRATION NUMBER: 42,891
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (412) 288-4192

Query Match Best Local Similarity Score 27; DB 3; Length 7;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
 Db 2 GVGVP 6

RESULT 15
 US-08-735-692-15
 ; Sequence 15, Application US/08735692B
 ; Patent No. 5972406
 ; GENERAL INFORMATION:
 ; APPLICANT: URRY, DAN W.
 ; APPLICANT: Sherry, Peter R.
 ; APPLICANT: Prasad, Kari
 ; TITLE OF INVENTION: Bielastomers Suitable as Food Product Additives
 ; FILE REFERENCE: BIEL/017/010US
 ; CURRENT APPLICATION NUMBER: US/08/735, 692B
 ; CURRENT FILING DATE: 1995-10-16
 ; EARLIER APPLICATION NUMBER: 08/423, 517
 ; EARLIER FILING DATE: 1995-04-14
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:synthetic

Query Match Best Local Similarity Score 27; DB 2; Length 15;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVGVP 5
 Db 11 GVGVP 15

Search completed: July 25, 2001, 16:49:57
 Job time: 68 sec

GenCore version 4.5
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4 protein - protein search, using sw model
 run on: July 25, 2001, 16:48:48 ; Search time 32.96 Seconds
 (without alignments)
 9.197 Million cell updates/sec

Title: US-09-251-638-1
 Perfect score: 27
 Sequence: 1 VPFGV 5

Scoring table: BLOSUM62
 Gapov 10.0 , Gapext 0.5

Searched: 412676 secs, 60623988 residues
 Total number of hits satisfying chosen parameters: 412676

Database : A_Geneseq_0601:
 1: /SIDS8/gcdata/geneseq/geneseq/AA1980.DAT: *
 2: /SIDS8/gcdata/geneseq/geneseq/AA1981.DAT: *
 3: /SIDS8/gcdata/geneseq/geneseq/AA1982.DAT: *
 4: /SIDS8/gcdata/geneseq/geneseq/AA1983.DAT: *
 5: /SIDS8/gcdata/geneseq/geneseq/AA1984.DAT: *
 6: /SIDS8/gcdata/geneseq/geneseq/AA1985.DAT: *
 7: /SIDS8/gcdata/geneseq/geneseq/AA1986.DAT: *
 8: /SIDS8/gcdata/geneseq/geneseq/AA1987.DAT: *
 9: /SIDS8/gcdata/geneseq/geneseq/AA1988.DAT: *
 10: /SIDS8/gcdata/geneseq/geneseq/AA1989.DAT: *
 11: /SIDS8/gcdata/geneseq/geneseq/AA1990.DAT: *
 12: /SIDS8/gcdata/geneseq/geneseq/AA1991.DAT: *
 13: /SIDS8/gcdata/geneseq/geneseq/AA1992.DAT: *
 14: /SIDS8/gcdata/geneseq/geneseq/AA1993.DAT: *
 15: /SIDS8/gcdata/geneseq/geneseq/AA1994.DAT: *
 16: /SIDS8/gcdata/geneseq/geneseq/AA1995.DAT: *
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 19: /SIDS8/gcdata/geneseq/geneseq/AA1998.DAT: *
 20: /SIDS8/gcdata/geneseq/geneseq/AA1999.DAT: *
 21: /SIDS8/gcdata/geneseq/geneseq/AA2000.DAT: *
 22: /SIDS8/gcdata/geneseq/geneseq/AA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	27	100.0	5	AAP61199 Repeating unit.
2	27	100.0	5	AAR29149 Pentapeptide repeat
3	27	100.0	5	AAR29145 Bioelastic pentapeptide
4	27	100.0	5	AAR65228 Fibrologen/beta-catenin
5	27	100.0	5	AAR80250 Elastin-like repeat
6	27	100.0	5	AAR80307 Elastin cross-link
7	27	100.0	5	AHW22714 Bioelastic core repeat
8	27	100.0	5	AHW26332 Elastin repeat unit
9	27	100.0	5	AHW18261 Transglutaminase
10	27	100.0	5	AHW21301 Monomer init factor
11	27	100.0	5	AHW49701 Elastin repeat motif

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

PR 19-SEP-1983; 83US-0533524.

ALIGNMENT S

RESULT 1
 AAP61199
 ID AAP61199 standard; Protein; 5 AA.
 XX
 AC AC1199;
 XX
 DT 01-AUG-1991 (first entry)
 XX
 DE Repeating unit.
 XY

XX	US4569882A.
PN	
XX	
	20-MAY-1986.
PD	
XX	
PF	19-SEP-1983;
XX	
	83US-0533524.

CC linking component. The copolymer is useful in prosthetic systems, for
 CC repairing a natural elastic system. It is so functionalised so as to
 CC provide reactive groups which can become covalently cross-linked by
 CC tissue enzymes to newly synthesised connective tissue protein.

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 vpgvg 5
 Db 1 vpgvg 5

RESULT 2
 AAR29149 standard; peptide; 5 AA.
 XX ID AAR29149;
 AC AAR29149;
 DT 06-MAY-1993 (first entry)
 DE Pentapeptide repeating unit of bioelastic polymer.
 XX Superabsorbent; bioelastic; diaper; hygienic articles; wound;
 XX dressing; implant; inverse temperature transition; tissue napkin;
 XX catbox liner; toilet paper; towellette; cleaning wipe; bandage;
 XX medical sponge; swab; printing ink; contact lens.
 OS Synthetic.

XX PN WO9218009-A.
 XX PR 29-OCT-1992.
 XX PD 10-MAR-1992; 92WO-US01959.

XX PF 19-APR-1991; 91US-0688185.

XX PA (BIOE-) BIOELASTICS RES LTD.

XX PI Urry DW; DR 1992-398469/48.

XX DR; 1992-381725/46.

XX PT Super-absorbent material incorporating polymer undergoing inverse
 PT temp. transition - esp. bio elastic polypeptide(s) for
 PT controllably absorbing body fluids.
 XX Claim 27/28; Page 34; 42pp; English.

XX The invention relates to an appliance suitable for contacting body
 CC surfaces and for absorbing aqueous liquids including body fluids.
 CC The appliance includes a polymeric material which undergoes an
 CC inverse temperature transition, pref. such that it is in a contracted state at a higher temperature and in a swollen state when at a lower temperature. The appliance, e.g. a diaper, may be selected to be in a contracted state prior to use and while contacting the body surface, and to be in a swollen state after absorbing a body fluid and being at a new location having a lower temperature distant from the body contacting location. Pref. the polymeric material is a bioelastic polymer containing elastomeric tetrapeptide, pentapeptide or nonapeptide repeat units, the polymer having a series of beta turns separated by dynamic bridging segments suspended between the beta turns. In particular, the polymer comprises a segment of formula poly((VPGVG)X(VPGVG)Y), in which X and Y are mole fractions such that x+y = 1, and X is a hydrophobic amino acid residue; or of formula poly((VPGVG)X(VPGVG)Y(VPGVG)Z), in which x+y+z = 1, X = as above, and Z is an amino acid residue having a side chain capable of undergoing reversible protonation in an aqueous environment.

CC A specific polymer is poly(vpgvg).
 XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VPGVG 5
 Db 1 vpgvg 5

RESULT 3
 AAR29145 standard; peptide; 5 AA.
 XX ID AAR29145;
 AC AAR29145;

DT 23-MAR-1993 (first entry)
 XX Bioelastic pentapeptide polymer fragment 2.
 DE XX
 DE Polymer fragment; inverse temperature transition; exerted pressure;
 KW mechanical work; chemical change; hydrophobicity.
 XX OS Synthetic.

XX PN WO9219183-A.
 XX PD 12-NOV-1992.
 XX PF 03-APR-1992; 92WO-US02691.
 XX PR 22-APR-1991; 91US-0688324.
 XX PA (UABR-) UAB RES FOUND.
 XX PI Urry DW;
 XX WPI; 1992-398469/48.

XX PT Pressure expanding polymers giving reversible mechanical changes
 PT - has inverse temp. transition in liq. water range and pref.
 PT being bio-elastic polypeptide(s) contg. hydrophobic gpts.
 XX PS Claims 13 and 14; Page 36; 51pp; English.
 XX CC The sequences given in AAR29144-46 are polymer fragments that are used
 CC in polymeric materials which have an inverse temp. transition in the
 CC range of liq. water and which expand against an exerted pressure.
 CC Fragments 1 and 2 are used such that mole fractions equal 1 in one
 CC polymeric material and fragments 1, 2 and 3 are used in a further
 CC polymeric material such that mole fractions equal 1. The materials
 CC can be used in a variety of applications to produce mechanical work
 CC and/or cause chemical changes in a sealed environment by variation of
 CC the pressure on the material. The degree of mechanical or chemical
 CC change can be controlled by selection of the number, hydrophobicity
 CC and size of the hydrophobic groups and the presence or absence of
 CC reactive functional groups in the polymer.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VPGVG 5
 Db 1 vpgvg 5

XX Cappello J;
 PI WPI: 1995-320413/41.
 DR XX
 Protein polymers comprising repeating units and sequences - capable
 PT of enzyme-catalysed covalent bond formation useful as a
 PT biocompatible material for wound closure and tissue repair
 XX Disclosure; Page 12; 138pp; English.

CC The sequence of the cross-linking reactive motif from elastin. The motif
 CC can be used in a novel polymer comprising two spaced enzyme recognition
 CC site and may contain repetitive units of 3-8 amino acids with at least
 CC two pendant groups. The polymers contg. the multimeric repeat sequence
 CC can be used as substrates for enzymatic cross-linking. The polymers can
 CC be used in biological systems where in situ formation of a biocompatible
 CC material with structural integrity is required e.g. as medical adhesives
 CC and sealants or for wound closure or tissue repair.
 XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
 Db 1 vpgvg 5

Sequence 5 AA;

Query Match 100.0%; Score 27; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
 Db 1 vpgvg 5

RESULT 7
 AAW22714 standard peptide; 5 AA.

XX AAW22714;

AC AC

XX DT 26-FEB-1998 (first entry)

DE Bioelastomeric repeating unit 1 responsive to electrical energy.

XX KW Bioelastomeric repeating unit; polymer; inverse temperature transition;

KW electrical energy change; polarity; hydrophobicity; mechanical work;

KW surgical suture; heat shrinkable membrane; desalination;

OS Synthetic.

XX PN WO9723729-A1.

PD 03-JUL-1997.

XX PD 07-JUN-1996; 96WO-US09776.

XX PR 07-JUN-1995; 95US-0487594.

PA (DRY/) DRY D W.

XX PI DRY DM;

XX DR WPI: 1997-363360/33.

PT Bioelastic polymer responsive to electrical energy - comprising
 PT side chain that changes polarity or hydrophobicity in response to electrical energy change, useful for
 PT mechanical work or light stimulated contraction
 XX Claim 13; Page 52; 60pp; English.

CC AAW22711-16 represent bioelastomeric repeating units that are used to
 CC create a polymer responsive to electrical energy. This bioelastic
 CC polymer comprises a bioelastomeric polypeptide having an inverse
 CC temperature transition, and a repeating bioelastomeric unit containing

XX at least 1 beta-turn and residues with a side chain. The side chain of
 CC these residues responds to an electrical energy change by altering its
 CC polarity or hydrophobicity. The side chain is present in sufficient
 CC amounts to provide a shift in the inverse temperature transition of the
 CC polymer upon the change in exposure to electrical energy. The polymer may
 CC also contain a second amino acid with a side chain capable of undergoing
 CC a change in an aqueous environment. The polymer (AAW3481-83) consists of
 CC the formulas described in AAW22716 and AAW22711 and below:
 CC Polyfix (VPGVG_nFV (VPDG)) where
 CC fx + fv = 1
 CC x represents an amino acid residue having an electrically responsive
 CC side chain.
 CC The expansion or contraction of the polymer upon exposure to a change
 CC in electrical energy can be used to produce mechanical work when the
 CC polymer is constrained. It can also cause turbidity and chemical changes
 CC in a closed environment. The polymer can be used in surgical sutures,
 CC especially for microsurgery, heat shrinkable membranes, controlled
 CC herbicide or pesticide release or for desalination.

SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
 Db 1 vpgvg 5

RESULT 8
 AAW26332

ID AAW26332 standard; Peptide; 5 AA.

XX AC AAW26332;

XX DT 19-NOV-1997 (first entry)

DE Elastin repeat unit.

XX KW Elastin; protein polymer.

XX Synthetic.

OS US5541648-A.

XX PN 24-JUN-1997.

XX PD 04-NOV-1986;

XX PF 86US-0927258.

XX PR 29-DEC-1993;

XX PR 93US-0175155.

XX PR 04-NOV-1986;

XX PR 86US-0927258.

XX PR 29-OCT-1987;

XX PR 87US-0114618.

XX PR 09-NOV-1988;

XX PR 88US-0269429.

XX PR 06-NOV-1990;

XX PR 90US-0609716.

XX PR 22-APR-1993;

XX PR 93US-0053049.

XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX PI Capello J, Ferrari FA, Richardson C;

XX DR WPI: 1997-340943/31.

PT Preparation of synthetic DNA encoding a protein comprising short
 PT repeats - by synthesising Oligomers, annealing and Oligomerising
 PT these, particularly to produce proteins that mimic silk, collagen
 PT etc

XX Claim 8; Column 11; 90pp; English.

CC This peptide represents a repeat unit found in elastin. Methods
 CC are claimed for preparing protein polymers that contain repeating

CC units based on those found in elastin, fibroin, keratin, etc. (see
 CC also AAW26329, AAW6334 and AAW26336). The method involves:
 CC synthesising pairs of single-stranded oligomers; each member of the pair
 CC overlapping except at the protruding ends; hybridising each pair to
 CC double-stranded segments; combining the double-stranded segments, or
 CC their cloned copies, in a cloning vector to form a monomer; excising
 CC the monomer from the vector; and oligomerising the monomer to
 CC produce a multimer. Such polymers comprise fibrous or structural
 CC proteins, including crystalline, elastomeric, tough and bony
 CC materials such as those that mimic (and can substitute for) silk,
 CC elastin, collagen, keratin etc. The properties of the protein can
 CC be controlled by varying the type of units in the monomer, the
 CC number of units per multimer, the spacing between them and the
 CC number of multimer repeats.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VPGVG 5
 Db 1 vpgvg 5

XX PS Claim 6; Page 48; 55PP; English.

XX PT Preparations.

XX PS Novel polypeptides optionally having one or both of the amino-terminus

CC and carboxy-terminus flanked by an elastomeric peptide, which is cross-

CC linked by a transglutaminase comprises a segment of formula:

CC S1-Y-S2. The present sequence represents a specifically claimed

CC example of an elastomeric peptide. The homo- and copolymers produced

CC are useful in tissue sealant and wound healing formulations. Tissue

CC sealants are useful in skin grafting for burn victims and for sealing

CC surgical and other wounds.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VPGVG 5
 Db 1 vpgvg 5

XX PS Novel polypeptides optionally having one or both of the amino-terminus

CC and carboxy-terminus flanked by an elastomeric peptide, which is cross-

CC linked by a transglutaminase comprises a segment of formula:

CC S1-Y-S2. The present sequence represents a specifically claimed

CC example of an elastomeric peptide. The homo- and copolymers produced

CC are useful in tissue sealant and wound healing formulations. Tissue

CC sealants are useful in skin grafting for burn victims and for sealing

CC surgical and other wounds.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VPGVG 5
 Db 1 vpgvg 5

RESULT 11

XX ID AAW49701 standard; Peptide; 5 AA;

Query Match 100.0%; Score 27; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VPGVG 5
 Db 1 vpgvg 5

RESULT 10
 ID AAW12301 standard; peptide; 5 AA.
 XX AC AAW12301;
 XX DT 22-APR-1997 (first entry)
 XX DE Monomeric unit for elastic protein-base polymer for chewing gum.
 XX KW Chewing gum; water; insoluble; plasticiser; elastomer; flavour; polymer;
 XX KW sweetener; texturiser; crosslinkage; gamma-irradiation; drug; nutrient;
 XX environment friendly; drug; anti-inflammatory agent; vitamin.
 XX OS Synthetic.
 XX PN US5580590-A.
 XX PD 03-DEC-1996.
 XX PF 27-DEC-1993; 93US-0174185.
 XX PR 27-DEC-1993; 93US-0174185.
 XX PA (WRIL) WRIGLEY JR CO WM.
 XX PI Hartman SE;
 XX DR WPI: 1997-033531/03.
 XX PT Environmentally friendly chewing gum - contg. water insoluble
 PT elastic polypeptide having a penta:peptide repeat
 XX PS Claim 1; Column 7; 6PP; English.
 XX CC A novel chewing gum composition comprises a water insoluble polymer
 CC comprising this pentapeptide as a base. The insoluble portion can
 CC comprise 1-9% of the gum, together with a plasticiser, an elastomer,
 CC a flavour, a sweetener and a texturiser. The peptide is preferably
 CC crosslinked by gamma-irradiation to form the polymer. The new chewing
 CC gum is environmentally friendly as it can be swallowed after chewing or
 CC easily removed from surfaces. The peptide can also have drugs or other
 CC nutrients e.g. anti-inflammatory agents, vitamins, etc., attached to the
 CC peptide, for therapeutic purposes.

Query Match 100.0%; Score 27; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 27; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VPGVG 5
 Db 1 vpgvg 5

RESULT 11

XX ID AAW49701 standard; Peptide; 5 AA;

Query Match 100.0%; Score 27; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VPGVG 5
 Db 1 vpgvg 5

DT 12-OCT-1998 (first entry)
 XX Elastin repeat motif.
 XX Protein polymer; cross-linking; elastin; adhesive; sealant;
 KW wound healing.
 XX Synthetic.
 OS
 XX US5773577-A.
 PN DR 12-MAR-1998.
 XX PD 23-SEP-1996; 96WO-US15306.
 XX PR 03-SEP-1996; 96US-0707237.
 XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 PN Cappello J, Crissman JW, Dorman MA, Ferrari FA;
 XX WPI; 1998-193613/17.
 XX PT Preparation of synthetic repetitive DNA - useful for construction of
 PT large protein polymers having repeating units, used in structural
 PT material; e.g. synthetic silk.
 XX PS Claim 11; Page 22; 127PP; English.
 XX This is the amino acid sequence of the peptide repeat unit, which
 CC is generally found in elastin, and used in the method of the invention.
 CC which involves the preparation of synthetic DNA sequence having
 CC repeating units from about 3-15 codons and encoding a protein of at
 CC least about 30 kDa. The method is useful for the production of high
 CC molecular weight polymers (e.g. synthetic silk), either nucleic acids
 CC or peptides that are the expression products of the nucleic acids and
 CC particularly high molecular weight peptides containing repeating units
 CC which are useful as structural materials.
 XX SQ Sequence 5 AA:
 Query Match 100.0%; Score 27; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPGVG 5
 DB 1 ||||| 5
 XX RESULT 4.13
 ID AAW47348
 ID AAW47348 standard; peptide; 5 AA.
 XX AC AAW47348;
 XX DT 01-JUN-1998 (first entry)
 XX DE Elastin repeat unit.
 XX KW Binding inhibitor; low-density lipoprotein; LDL; vascular wall;
 KW vascular disease; elastin; collagen; prevention; treatment;
 XX Homo sapiens.
 XX OS
 PN US5726153-A.
 XX PD 10-MAR-1998.
 XX PF 06-JUN-1995;
 XX PR 06-JUN-1995;
 XX PR 06-JUN-1995;
 XX PR 02-MAY-1998;
 XX PR 03-MAY-1990;
 KW 90US-0518215;
 KW PR 02-MAY-1991;
 KW 91US-0694929;
 KW PR 16-APR-1993;
 KW 93US-0048569;
 KW PR 24-FEB-1994;
 KW PR 28-FEB-1995;
 KW PR 06-JUN-1995;
 KW 95US-0468543.
 XX Peptide repeat unit 4.
 XX Peptide repeat unit; DNA repeat unit; high molecular weight polymer;
 KW synthetic silk; silk worm; elastin.
 OS
 XX Synthetic.
 OS Bombyx mori.
 PN WO9810063-A1.

PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
 XX
 PI Fischman A, Lees AM, Lees RS, Shih I;
 XX
 WPI: 1998-192802/17.
 XX
 Inhibiting binding of low-density lipoprotein to vascular walls - by
 PT administering peptide with affinity for vascular injury sites
 XX
 PS Disclosure: Column 14; 31pp; English.
 XX
 CC A novel method for inhibiting the binding of a low-density
 CC lipoprotein (LDL) to vascular walls in vivo, comprises
 CC administering a synthetic water soluble peptide containing an
 CC amphiphilic domain and having affinity for sites of vascular
 CC injury, e.g., derived from the present peptide.
 CC The peptide inhibits the binding of LDL to vascular wall
 CC components, e.g., elastin and collagen, and so can be used to
 CC prevent or treat vascular diseases, e.g., atherosclerosis.
 XX
 Sequence 5 AA;

Query Match Score 27; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 VPGVG 5
 Db 1 vpgvg 5

RESULT 14
 AAY558577 Standard; Peptide; 5 AA.
 ID AAY558577
 XX
 AC AAY558577;
 XX
 DT 01-FEB-2000 (first entry)
 XX
 DE Apolipoprotein fragment peptide #27 for vascular disease imaging.
 XX
 KW Diagnosis; water soluble; amphiphilic domain; affinity; vascular injury;
 KW detection; imaging; disease; atherosclerosis; apolipoprotein.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5972890-A.
 XX
 PD 26-OCT-1999.
 XX
 PF 28-FEB-1995; 95US-0398046.
 XX
 PR 02-MAY-1991; 91US-0694922.
 PR 16-APR-1993; 93US-0048559.
 PR 24-FEB-1994; 94US-0201057.
 PR 02-MAY-1988; 88US-0189110.
 PR 03-MAY-1990; 90US-0518112.
 PR 03-MAY-1990; 90US-0518215.
 PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
 XX
 PT Lees AM, Fischman A, Shih I, Findeis MA, Lees RS;
 XX
 DR WPI: 1999-632641/54.
 XX
 PT New diagnostic synthetic peptides which have affinity for and
 PT accumulate at a site of vascular injury useful for detection and
 PT imaging of vascular disease such as atherosclerosis -
 XX
 PS Claim 37; Column 34; 30pp; English.
 XX

CC The peptides AAY558577-1955889 represent examples of diagnostic, synthetic
 CC peptides which carry a detectable label, contain 30 or fewer amino
 CC acids, are water soluble, contain an amphiphilic domain and have affinity
 CC for, and propensity to accumulate at, a site of vascular injury. They
 CC are preferably derived from the amino acid sequence of apolipoprotein.
 CC The peptides can be used for the detection or imaging of a vascular
 CC injury or disease, e.g., atherosclerosis.
 XX
 SQ Sequence 5 AA;

Query Match Score 27; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 VPGVG 5
 Db 1 vpgvg 5

RESULT 15
 AAV31686 Standard; Peptide; 5 AA.
 ID AAV31686
 XX
 AC AAV31686;
 XX
 DT 22-NOV-1999 (first entry)
 XX
 DE Pentapeptide used in novel elastomer polymers.
 XX
 KW Elastomer; bioelastomer; polymer; tissue augmentation;
 KW tissue restoration; tissue repair; implant.
 XX
 OS Synthetic.
 XX
 PN WO943271-A1.
 XX
 PD 02-SEP-1999.
 XX
 PF 26-FEB-1999; 99WO-US04440.
 XX
 PR 29-MAY-1998; 98US-0087155.
 PR 27-FEB-1998; 98US-0076297,
 XX
 PA (BIOE-) BIOELASTICS RES LTD.
 XX
 PI Glazer PA, Parker TM, Urry DW;
 XX
 DR WPI; 1999-540487/45.

Claim 9; Page 75; 133pp; English.

PT Augmentation or restoration of mammalian tissue by injecting
 PT solution of peptide polymer, used for soft or hard tissue
 PT reconstruction, especially of intervertebral disks
 XX
 PS The present sequence represents an example of a pentapeptide that
 CC is used in novel bioelastic polymers. The invention provides a
 CC method of tissue augmentation by injecting a polymer comprising
 CC repeating peptide monomeric units selected from nonapeptide,
 CC pentapeptide and tetrapeptide monomeric units, where the monomeric
 CC units form a series of beta-turns separated by dynamic bridging
 CC segments. The polymer has an inverse temperature transition value
 CC that is less than the tissue temp. and is injected in water
 CC solution at coacervate concentration. The polymer can be injected
 CC at periurethral or subdermal sites (for treatment of urinary
 CC incontinence or for cosmetic purposes), or into hard or soft
 CC tissue, e.g., for repair of traumatic injury. A specific
 CC application is restoration of intervertebral discs.
 XX
 SQ Sequence 5 AA;

```
Query Match      100.0%;  SCORE 27;  DB 20;  Length 5;
Best Local Similarity 100.0%;  Pred. No. 3.4e+05;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;
Gaps 0;

Qy   1 VPGVG 5
      |||||
Db   1 vpgvrg 5
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Search completed: July 25, 2001, 16:49:30
Job time: 42 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 25, 2001, 16:48:49 ; Search time 20.09 seconds
(without alignments)
5.125 Million cell updates/sec

Title: US-09-251-638-1
Perfect score: 27
Sequence: 1 VPGVG 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Issued Patents AA:
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 4: /cgn2_6/ptcdata/1/1aa/6B_COMB_pep:
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 6: /cgn2_6/ptcdata/1/1aa/backfile1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	27	100.0	5	1	US-08-106-509-5	Sequence 5, Appli
2	27	100.0	5	1	US-07-609-716-2	Sequence 2, Appli
3	27	100.0	5	1	US-08-174-185-1	Sequence 1, Appli
4	27	100.0	5	1	US-08-212-237-2	Sequence 2, Appli
5	27	100.0	5	1	US-08-175-155-4	Sequence 4, Appli
6	27	100.0	5	1	US-08-175-155-9	Sequence 9, Appli
7	27	100.0	5	1	US-08-168-543-15	Sequence 15, Appli
8	27	100.0	5	1	US-08-477-509B-24	Sequence 24, Appli
9	27	100.0	5	1	US-08-397-633A-1	Sequence 1, Appli
10	27	100.0	5	1	US-08-397-633A-8	Sequence 8, Appli
11	27	100.0	5	2	US-08-707-237A-10	Sequence 10, Appli
12	27	100.0	5	2	US-08-483-236-15	Sequence 15, Appli
13	27	100.0	5	2	US-08-692-15	Sequence 15, Appli
14	27	100.0	5	2	US-08-911-366-6	Sequence 6, Appli
15	27	100.0	5	2	US-08-735-692-20	Sequence 20, Appli
16	27	100.0	5	2	US-08-598-045-15	Sequence 15, Appli
17	27	100.0	5	3	US-08-542-051-1	Sequence 1, Appli
18	27	100.0	5	3	US-08-48-085B-24	Sequence 24, Appli
19	27	100.0	5	3	US-08-05B-43	Sequence 43, Appli
20	27	100.0	5	3	US-08-263-168C-27	Sequence 27, Appli
21	27	100.0	5	4	US-08-475-41A-2	Sequence 2, Appli
22	27	100.0	5	4	US-08-178-029A-2	Sequence 2, Appli
23	27	100.0	5	5	PCT-US95-02772-2	Sequence 2, Appli
24	27	100.0	5	6	5230516-1	Patent No. 5230516
25	27	100.0	5	6	5230516-17	Patent No. 5230516
26	27	100.0	6	1	US-08-468-543-12	Sequence 12, Appli
27	27	100.0	6	2	US-08-469-692-12	Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-08-106-509-5
; Sequence 5, Application US/08106509
; Patent No. 5428014
; GENERAL INFORMATION:
; APPLICANT: Labbro, Virender
; TITLE OF INVENTION: TRANSGLUTAMINASE CROSS-LINKABLE
; PEPTIDES AND METHODS RELATING THERETO
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,509
; FILING DATE: 19930813
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-684
; REFERENCE/DOCKET NUMBER: 93-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-106-509-5

Query Match Best Local Similarity Score 27; DB 1; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
Db 1 VPGVG 5

RESULT ²
 US-07-609-716-2
 Sequence 2, Application US/07609716
 Patent No. 5514581
 GENERAL INFORMATION:
 APPLICANT: Ferrai, Franco A.
 APPLICANT: Cappello, Joseph
 TITLE OF INVENTION: Functional Recombinantly Prepared
 NUMBER OF SEQUENCES: 118
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: CA
 COUNTRY: US
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/609,716
 FILING DATE: 06-NOV-1990
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertram I.
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: A-551186-3/BIR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-07-609-716-2

MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/174,185
 FILING DATE: 27-DEC-1993
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acid residues
 TYPE: amino acid
 STRANDEDNESS: N/A
 TOPOLOGY: N/A
 MOLECULE TYPE: peptide
 US-08-174-185-1

Query Match 100.0%; Score 27; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT ⁴
 US-08-212-237-2
 Sequence 2, Application US/08212237
 Patent No. 5606019
 GENERAL INFORMATION:
 APPLICANT: Cappello, Joseph
 TITLE OF INVENTION: Synthetic Proteins As Implantables
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/212,237
 FILING DATE: 11-MAR-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertram I.
 REGISTRATION NUMBER: 20,015
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-212-237-2

Query Match 100.0%; Score 27; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT ³
 US-08-174-185-1
 Sequence 1, Application US/08174185
 Patent No. 5,880590
 GENERAL INFORMATION:
 APPLICANT: Hartman, Scott E.
 TITLE OF INVENTION: Environmentally Friendly
 CHEWING GUM COMPOSITIONS CONTAINING ELASTIC PROTEIN-BASED
 TITLE OF INVENTION:
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hill, Steedman & Simpson
 STREET: 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb

Query Match 100.0%; Score 27; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
 |||||

Db 1 VPGVG 5

RESULT 5

US-08-175-155-4

Sequence 4 , Application US/08175155

; Patent No. 5641648

; GENERAL INFORMATION:

; APPLICANT: Ferrari, Franco A.

; ATTORNEY: Cappello, Joseph

; Crissman, John W.

; APPLICANT: Dorman, Mary A.

; TITLE OF INVENTION: Methods for Preparing Synthetic

; TITLE OF INVENTION: Repetitive DNA

; NUMBER OF SEQUENCES: 69

; CURRENT APPLICATION DATA:

; ADDRESSSEE: Fiehr, Hohbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: US

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/175,155

; FILING DATE: 29-DEC-1993

; CLASSIFICATION: 435

; TELECOMMUNICATION INFORMATION:

; NAME: Rowland, Bertram I.

; REGISTRATION NUMBER: 20015

; REFERENCE/DOCKET NUMBER: A-551186-5/BIR

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-781-1989

; TELEFAX: 415-398-3249

; INFORMATION FOR SEQ ID NO: 4 :

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-175-155-9

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/175,155

; FILING DATE: 29-DEC-1993

; CLASSIFICATION: 435

; TELECOMMUNICATION INFORMATION:

; NAME: Rowland, Bertram I.

; REGISTRATION NUMBER: 20015

; REFERENCE/DOCKET NUMBER: A-551186-5/BIR

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-781-1989

; TELEFAX: 415-398-3249

; INFORMATION FOR SEQ ID NO: 4 :

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-175-155-4

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/175,155

; FILING DATE: 29-DEC-1993

; CLASSIFICATION: 435

; TELECOMMUNICATION INFORMATION:

; NAME: Rowland, Bertram I.

; REGISTRATION NUMBER: 20015

; REFERENCE/DOCKET NUMBER: A-551186-5/BIR

; TELECOMMUNICATION INFORMATION:

; NAME: Rowland, Bertram I.

; REGISTRATION NUMBER: 20015

; REFERENCE/DOCKET NUMBER: A-551186-5/BIR

; TELECOMMUNICATION INFORMATION:

; NAME: Rowland, Bertram I.

; REGISTRATION NUMBER: 20015

; REFERENCE/DOCKET NUMBER: A-551186-5/BIR

; TELECOMMUNICATION INFORMATION:

; NAME: Rowland, Bertram I.

; REGISTRATION NUMBER: 20015

; REFERENCE/DOCKET NUMBER: A-551186-5/BIR

; TELECOMMUNICATION INFORMATION:

; NAME: Rowland, Bertram I.

; REGISTRATION NUMBER: 20015

; REFERENCE/DOCKET NUMBER: A-551186-5/BIR

; TELECOMMUNICATION INFORMATION:

; NAME: Rowland, Bertram I.

;

STATE: CA

COUNTRY: US

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Bertram I.

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A-551186-5/BIR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-398-3249

TELEFAX: 415-781-1989

INFORMATION FOR SEQ ID NO: 9 :

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-175-155-15

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/175,155

FILING DATE: 29-DEC-1993

CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:

NAME: Rowland, Bertram I.

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A-551186-5/BIR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-398-3249

TELEFAX: 415-781-1989

INFORMATION FOR SEQ ID NO: 9 :

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-175-155-9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/175,155

FILING DATE: 29-DEC-1993

CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:

NAME: Rowland, Bertram I.

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A-551186-5/BIR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-398-3249

TELEFAX: 415-781-1989

INFORMATION FOR SEQ ID NO: 9 :

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-175-155-15

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/175,155

FILING DATE: 29-DEC-1993

CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:

NAME: Rowland, Bertram I.

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A-551186-5/BIR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-398-3249

TELEFAX: 415-781-1989

INFORMATION FOR SEQ ID NO: 9 :

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-175-155-9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/175,155

FILING DATE: 29-DEC-1993

CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:

NAME: Rowland, Bertram I.

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A-551186-5/BIR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-398-3249

TELEFAX: 415-781-1989

INFORMATION FOR SEQ ID NO: 9 :

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-175-155-9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/175,155

FILING DATE: 29-DEC-1993

CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:

NAME: Rowland, Bertram I.

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A-551186-5/BIR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-398-3249

TELEFAX: 415-781-1989

INFORMATION FOR SEQ ID NO: 9 :

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-175-155-9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/175,155

FILING DATE: 29-DEC-1993

CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:

NAME: Rowland, Bertram I.

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A-551186-5/BIR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-398-3249

TELEFAX: 415-781-1989

INFORMATION FOR SEQ ID NO: 9 :

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-175-155-9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/175,155

FILING DATE: 29-DEC-1993

CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:

NAME: Rowland, Bertram I.

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A-551186-5/BIR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-398-3249

TELEFAX: 415-781-1989

INFORMATION FOR SEQ ID NO: 9 :

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-175-155-9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/175,155

FILING DATE: 29-DEC-1993

CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:

NAME: Rowland, Bertram I.

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A-551186-5/BIR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-398-3249

TELEFAX: 415-781-1989

INFORMATION FOR SEQ ID NO: 9 :

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-175-155-9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/175,155

FILING DATE: 29-DEC-1993

CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:

NAME: Rowland, Bertram I.

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A-551186-5/BIR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-398-3249

TELEFAX: 415-781-1989

INFORMATION FOR SEQ ID NO: 9 :

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-175-155-9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/175,155

PATENT APPLICATION DATA:
 FILING DATE: 02-MAY-1991
 APPLICATION NUMBER: US 07/518,215
 FILING DATE: 03-MAY-1990
 PATENT APPLICATION DATA:
 APPLICATION NUMBER: US 07/518,142
 FILING DATE: 03-MAY-1990
 PATENT APPLICATION DATA:
 APPLICATION NUMBER: US 07/189,130
 FILING DATE: 02-MAY-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30 162
 REFERENCE/DOCKET NUMBER: 04547/002003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
 US-08-468-543-15

Query Match Score 27; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 US-08-477-509B-24
 Sequence 24, Application US/08477509B
 GENERAL INFORMATION:
 PATENT NO. 570697
 APPLICANT: Ferrari, Franco A
 APPLICANT: Cappello, Joseph A
 APPLICANT: Crissman, John W
 APPLICANT: Dorman, Mary A
 TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
 NUMBER OF SEQUENCES: 112
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Rohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 ZIP: 94111
 COUNTRY: US

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,509B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/175,155
 FILING DATE: 29-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/053,049
 FILING DATE: 22-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/114,618
 FILING DATE: 29-OCT-1987

PATENT APPLICATION DATA:
 APPLICATION NUMBER: US 06/927,258
 FILING DATE: 04-NOV-1986
 ATTORNEY/AGENT INFORMATION:
 NAME: Trecartin, Richard F.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-477-509B-24

Query Match Score 27; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPGVG 5
 Db 1 VPGVG 5

RESULT 9
 US-08-397-632A-1
 Sequence 1, Application US/08397633A
 ; Patent No. 5773577
 ; GENERAL INFORMATION:
 ; APPLICANT: Cappello, Joseph
 ; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATES CAPABLE
 ; OF ENZYMATIC CROSS-LINKING
 ; NUMBER OF SEQUENCES: 105
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLEHR, ROHBACH, TEST, ALBRITTON & HERBERT
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/397,633A
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20,015
 ; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Peptide
 US-08-397-632A-1

Query Match Score 27; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
 Db 1 VPGVG 5

RESULT 10
 US-08-397-633A-8
 Sequence 8, Application US/08397633A
 Patent No. 5773577
 GENERAL INFORMATION:
 APPLICANT: Cappello, Joseph
 TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATECAPABLE
 NUMBER OF SEQUENCES: 105
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLEHR, HOIBACH, TEST, ALBRITTON & HERBERT
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/397,633A
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertam I
 REGISTRATION NUMBER: 20,015
 REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-397-633A-8

Query Match 100.0%; Score 27; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
 Db 1 VPGVG 5

RESULT 11
 US-08-707-237A-10
 Sequence 10, Application US/08707237A
 Patent No. 583013
 GENERAL INFORMATION:
 APPLICANT: Ferrari, Franco A.
 APPLICANT: Capello, Joseph
 APPLICANT: Crisman, John W.
 APPLICANT: Dorman, Mary A.
 TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC
 NUMBER OF SEQUENCES: 108
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics, Inc.
 STREET: 1201 Eastlake Avenue East

ADDRESSEE: Flehr, Hoibach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-1187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/707,237A
 FILING DATE: 03-SEP-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/175,155
 FILING DATE: 29-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/053,049
 FILING DATE: 22-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/609,716
 FILING DATE: 06-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/269,429
 FILING DATE: 09-NOV-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/114,618
 FILING DATE: 29-OCT-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/927,258
 FILING DATE: 04-NOV-1986
 ATTORNEY/AGENT INFORMATION:
 NAME: Trecartin, Richard F.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-55186-10/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-707-237A-10

Query Match 100.0%; Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
 Db 1 VPGVG 5

RESULT 12
 US-08-483-236-15
 Sequence 15, Application US/08483236
 Patent No. 5939385
 GENERAL INFORMATION:
 APPLICANT: Labroo, Virender
 APPLICANT: Busby, Sharon
 TITLE OF INVENTION: Transglutaminase Cross-Linkable
 Peptides and Methods Relating Thereto
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics, Inc.
 STREET: 1201 Eastlake Avenue East

; TELEFAX: (202) 672-5399
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-911-364-6

Query Match 15 Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VPGVG 5
 Db 1 VPGVG 5

RESULT 15
 US-08-735-692-20
 ; Sequence 20, Application US/08735692B
 ; Patent No. 5972406
 ; GENERAL INFORMATION:
 ; APPLICANT: Urry, Dan W.
 ; APPLICANT: Shevry, Peter R.
 ; APPLICANT: Presad, Kari
 ; TITLE OF INVENTION: Bielastomers Suitable as Food Product Additives
 ; FILE REFERENCE: BERL-017/01US
 ; CURRENT APPLICATION NUMBER: US/08/735,692B
 ; EARLIER APPLICATION NUMBER: 08/423,517
 ; CURRENT FILING DATE: 1995-10-16
 ; EARLIER FILING DATE: 1995-04-14
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 20
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:synthetic
 US-08-735-692-20

Query Match 15 Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VPGVG 5
 Db 1 VPGVG 5

Search completed: July 25, 2001, 16:49:56
 Job time: 67 sec

CITY: Seattle
 STATE: WA
 ZIP: 98102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,236
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Parker, Gary E.
 REGISTRATION NUMBER: 31-648
 REFERENCE/DOCKET NUMBER: 93-09c1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6673
 TELEX: 206-442-6678
 FAX: 206-442-6678
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-483-236-15

Query Match Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 VPGVG 5
 |||||
 Db 1 VPGVG 5

RESULT 13
 US-08-469-692-15
 Sequence 15, Application US/08469692
 Patent No. 555055
 GENERAL INFORMATION:
 APPLICANT: Lees, Robert S. et al.
 TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR ARTERIAL IMAGING
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,692
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/398,046
 FILING DATE: 02-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/201,057
 FILING DATE: 24-FEB-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/048,569
 FILING DATE: 16-APR-1993
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/694,929
 FILING DATE: 02-MAY-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/518,215
 FILING DATE: 03-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/518,142
 FILING DATE: 03-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/189,130
 FILING DATE: 02-MAY-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30-162
 REFERENCE/DOCKET NUMBER: 04547/002002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-469-692-15

Query Match Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 VPGVG 5
 |||||
 Db 1 VPGVG 5

RESULT 14
 US-08-911-364-6
 Sequence 6, Application US/08911364
 Patent No. 5969106
 GENERAL INFORMATION:
 APPLICANT: ROTSTEIN, Aser
 APPLICANT: KEELY, Fred W.
 APPLICANT: ROTSTEIN, Steven J.
 TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN
 TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY & LARDNER
 STREET: 3000 K Street, N.W.
 CITY: Washington
 STATE: D.C.
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/911,364
 FILING DATE: 07-AUG-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/023,552
 FILING DATE: 07-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Bent, Stephen A.
 REGISTRATION NUMBER: 29-7768
 REFERENCE/DOCKET NUMBER: 041082/0104
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300

Gencore version 4.5
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OW protein - protein search, using sw model

Run on: July 25, 2001, 16:48:49 ; Search time 22.51 Seconds
(without alignments)
16.920 Million cell updates/sec

Title: US-09-251-638-1

Perfect score: 27

Sequence: 1 VPVG 5

Scoring table: BLOSSM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:
1: P1r1:
2: P1r2:
3: P1r3:
4: P1r4:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	38	T4593	phytoene dehydrogenase
2	27	100.0	76	I45885	elastin - bovine (hypothetical prote
3	27	100.0	93	C40595	hydrogenase express
4	27	100.0	120	A75586	hypothetical prote
5	27	100.0	127	A72712	hypothetical prote
6	27	100.0	139	C70680	hypothetical prote
7	27	100.0	162	G96671	hypothetical prote
8	27	100.0	170	BB3664	hypothetical prote
9	27	100.0	181	T05925	hypothetical prote
10	27	100.0	195	G64359	adenylate kinase (hypothetical prote
11	27	100.0	199	E6534	DNA polymerase, ba
12	27	100.0	204	E72695	adenylate kinase (probable amidotran
13	27	100.0	206	D70544	probable amidotran
14	27	100.0	206	T45249	probable two-compo
15	27	100.0	213	T36699	hypothetical prote
16	27	100.0	214	T23593	glutamine amidotra
17	27	100.0	222	JQ0640	hypothetical prote
18	27	100.0	231	D72532	hypothetical prote
19	27	100.0	246	T37169	hypothetical prote
20	27	100.0	255	A70778	hypothetical prote
21	27	100.0	267	G84319	orotidine-5'-monop
22	27	100.0	271	S76871	hypothetical prote
23	27	100.0	274	G70898	orotidine-5'-phosp
24	27	100.0	274	B49930	hypothetical prote
25	27	100.0	281	G70734	poly(3-hydroxyalika
26	27	100.0	283	B38604	poly(3-hydroxyalika
27	27	100.0	285	S29307	conserved hypothet
28	27	100.0	293	B75441	conserved hypothet
29	27	100.0	294	E69968	conserved hypothet

ALIGNMENTS

RESULT	1	Query Match Similarity 100.0%; Score 27; DB 2; Length 38; Pred. No. 37; Mismatches 0; Indels 0; Gaps 0;					
T46593	phytoene dehydrogenase [imported] - Mycobacterium marinum (fragment)						
C;Species: Mycobacterium marinum							
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000							
C;Accession: T46593							
R;Ramaskrishnan, L.; Tran, H.T.; Fedderspiel, N.A.; Falkow, S.							
J;Title: A crtB homolog essential for Photochromogenicity in Mycobacterium marinum: i							
A;Reference number: 223096; MUID:97440138							
A;Status: Preliminary; translated from GB/EMBL/DDJB							
A;Accession: T6593							
A;Molecule type: DNA							
A;Residues: 1-38 <RAM>							
A;Cross-references: ENBL:U92075; NID:91928930; PIDN:AAB71427.1; PID:91928931							
A;Experimental source: strain M							
C;Genetics:							
A;Gene:	crtB						

Qy 1 VPGVG 5
Db 34 VPGVG 38

RESULT 3
c40595
hypothetical protein (mutB 3' region) - Streptomyces cinnamomensis (fragment)
C;Species: Streptomyces cinnamomensis
C;Accession: 03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Feb-1995
C;Accession: C40595
R;Birch, A.; Leiser, A.; Robinson, J.A.
A;Title: Cloning, sequencing, and expression of the gene encoding methylmalonyl-coenzyme-A;Reference number: A40595; MUID:93273720

Qy 1 VPGVG 5
Db 41 VPGVG 45

Query Match 100.0%; Score 27; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
A75586
hydrogenase expression/formation HPA-related protein - Deinococcus radiodurans (strain R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Smith, H.O.; Ventre, J.C.; Fraser, C.M.
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75520; MUID:20056896
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE001825; PID:96460670; PID:9646075
A;Experimental source: strain R1
A;Gene: DRA0316
A;MAP position: 2
C;Superfamily: hydrogenase accessory protein

Qy 1 VPGVG 5
Db 67 VPGVG 71

Query Match 100.0%; Score 27; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
A72712
hypothetical protein APE1112 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: A72712

R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.
DNA Res. 6, 93-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero

A;Reference number: A72450; MUID:99310339
A;Accession: A72712
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-127 <KAW>
A;Cross-references: DBJ:AP000060; NTDB:95104188; PIDN:BAA80097.1; PIDN:di1043883; PID:95104188
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1112
C;Superfamily: Aeropyrum pernix hypothetical protein APE1112

Qy 1 VPGVG 5
Db 19 VPGVG 23

Query Match 100.0%; Score 27; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
C70800
hypothetical protein Rv2437 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Accession: C70800
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Cole, S.T.; Brooch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Connor, R.; Davies, R.; Feltwell, P.; Gentles, S.; Hamlin, N.; Holloway, R.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Accession: A70500; MUID:98295987
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-139 <COL>
A;Cross-references: GB:281451; GB:AL123456; NID:93261662; PIDN:CARB03782.1; PID:ee28049
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: RV2437

Qy 1 VPGVG 5
Db 132 VPGVG 136

Query Match 100.0%; Score 27; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
G96671
hypothetical protein F13011.15 (imported) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse ear cress)
C;Accession: G96671
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Rheologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewar, N.E.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Liu, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurie, J.S.; Maiti, R.; Marzella, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719
 A; Accession: G96671
 A; Status: Preliminary
 A; Molecule type: DNA
 A; Residues: 1-162 <STO>
 A; Cross-references: GB:AE005173; NID:95042420; PIDN:AAD38259.1; GSPDB:GN00141
 C; Genetics:
 A; Gene: F13C01.15
 A; Map position: 1
 Db 120 VPGVG 124

RESULT 10
 G64359
 adenylate kinase (EC 2.7.4.3) MJ0479 [similarity] - Methanococcus jannaschii
 C; Species: Methanococcus jannaschii
 C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C; Accession: G64359
 R; Built, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
 r, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,
 rson, J.D.; Sodow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 105-1073, 1996
 A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.O.; Fraser, C.M.; Smith, H.O.; Woese
 C; Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*
 A; Reference number: A64300; MUID:96337909
 A; Status: Preliminary: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-195 <BUL>
 A; Cross-references: GB:U67498; GB:L77117; NID:91591180; PIDN:AAB98470.1; PID:91591182
 C; Genetics:
 A; Map position: FR0421829-422416
 A; Start codon: GTG
 C; Superfamily: Sulfolobus adenylate kinase
 C; Keywords: phosphotransferase

Query Match 100.0%; Score 27; DB 2; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
 Db 131 VPGVG 135

RESULT 8
 BB3664
 hypothetical protein BH0114 [imported] - *Bacillus halodurans* (strain C-125)
 C; Species: *Bacillus halodurans*
 C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
 C; Accession: B83664
 R; Takami, H.; Nakasone, K.; Takiaki, Y.; Maeno, G.; Sasakai, R.; Masui, N.; Fujii, F.; Hirai
 Nucleic Acids Res. 28, 4317-4331, 2000
 A; Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A; Reference number: AB3650; MUID:20263314
 A; Accession: B83664
 A; Status: Preliminary
 A; Molecule type: DNA
 A; Residues: 1-170 <STO>
 A; Cross-references: GB:AP001507; NID:BA000004; PIDN:g10172612; PIDN:BA03333.1; GSPDB:GN00
 A; Experimental source: strain C-125
 C; Genetics:
 A; Gene: BH0114

RESULT 11
 B69334
 DNA polymerase, bacteriophage-type homolog - *Archaeoglobus fulgidus*
 C; Species: *Archaeoglobus fulgidus*
 C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999
 C; Accession: B69334
 R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.S.; Gill, S.; Kirkness, E
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; McDonald, J.F.; McDaniel, L.
 Nature 390, 364-370, 1997
 A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
 A; Reference number: A69350; MUID:98049943
 A; Accession: B69334
 A; Status: Preliminary: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-199 <RLE>
 A; Cross-references: GB:AE000947; PIDN:92689270; PIDN:ABB88977.1; PID:9264
 C; Superfamily: Archaeoglobus probable DNA-polymerase

Query Match 100.0%; Score 27; DB 2; Length 199;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
 Db 27 VPGVG 31

RESULT 12
 E7295
 adenylate kinase (EC 2.7.4.3) APE0981 [similarity] - *Aeropyrum pernix* (strain K1)
 C; Species: *Aeropyrum pernix*
 C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

Query Match 100.0%; Score 27; DB 2; Length 181;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
 Db 27 VPGVG 31

C;Accession: E72695
 R;Kavano, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; takahawa, H.; Takamya, M.; Nasuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; kDNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
 A;Reference number: A72450; M01D:99310339
 A;Accession: E72695
 A;Molecule type: DNA
 A;Residues: 1-204 <RAW>
 A;Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BAA79965.1; PID:95104650
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: AP0981
 C;Superfamily: sulfolobus adenylyl kinase
 C;Keywords: phosphotransferase

RESULT 15

Query	Match	Score	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Qy 1 VPGVG 5 Db 15 VPGVG 19	T36699 probable amidotransferase - Streptomyces coelicolor (fragment) C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000 C;Accession: T36699 R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. A;Reference number: Z21597 A;Accession: T36699 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-213 <MUR>	100.0%	204	100.0%	2e+02	0	0	0

D70544
 probable amidotransferase - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C;Accession: D70544
 R;Cole, S.T.; Brosch, R.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Faltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutitter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature, 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Accession number: A70500; M01D:98295987
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-206 <COL>
 A;Cross-references: GB:295586; GB:AU123456; NID:g3261785; PIDN:CAB09092.1; PID:q2117235
 C;Genetics:
 A;Gene: hsh
 C;Superfamily: amidotransferase hsh; trpG homology

Search completed: July 25, 2001, 16:50:26
 Job time: 97 sec

RESULT 13

Query	Match	Score	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Qy 1 VPGVG 5 Db 15 VPGVG 19	D70544 probable amidotransferase - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: D70544 R;Cole, S.T.; Brosch, R.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Faltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutitter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature, 393, 537-544, 1998 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession number: A70500; M01D:98295987 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-206 <COL> A;Cross-references: GB:295586; GB:AU123456; NID:g3261785; PIDN:CAB09092.1; PID:q2117235 C;Genetics: A;Gene: hsh C;Superfamily: amidotransferase hsh; trpG homology	100.0%	204	100.0%	2e+02	0	0	0

Qy 1 VPGVG 5
Db 15 VPGVG 19

Query Match Score 27 DB 2 Length 206;
 Best Local Similarity 100.0% Pred. No. 2e+02;
 Matches 5 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
Db 47 VPGVG 51

Query Match Score 27 DB 2 Length 206;
 Best Local Similarity 100.0% Pred. No. 2e+02;
 Matches 5 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
Db 47 VPGVG 51

RESULT 14

Query	Match	Score	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Qy 1 VPGVG 5 Db 47 VPGVG 51	T45249 probable amidotransferase [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000 C;Accession: T45249 R;James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. A;Reference number: Z22949 A;Accession: T45249 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-206 <JAM>	100.0%	206	100.0%	2e+02	0	0	0

Scoring table:	BLOSUM62						
Gapopen:	10.0						
Gapext:	0.5						
Searched:	93435 seqs, 34255486 residues						
Total number of hits satisfying chosen parameters:	93435						
Minimum DB seq length:	0						
Maximum DB seq length:	2000000000						
Post-processing:	Minimum Match 0%						
	Maximum Match 100%						
	Listing first 45 summaries						
Database :	SwissProt_39;*						
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
	SUMMARIES						
Result No.	Score	Query	Match	Length	DB	ID	Description
1	27	100.0	93	1	YMU3_STROM		Q5072 streptomyce
2	27	100.0	128	1	COXE_CAEEL		Q20779 caenorhabdi
3	27	100.0	181	1	Y65L_HORVU		Q4609 hordeum vul
4	27	100.0	192	1	KADA_METTA		P42408 methanococc
5	27	100.0	192	1	KADA_METTL		P42409 methanococc
6	27	100.0	192	1	KADA_METTO		P42410 methanococc
7	27	100.0	192	1	KADA_AERPE		P93d2 aeroprum P
8	27	100.0	204	1	HIS5_MYCIE		Q957c0 mycobacteri
9	27	100.0	206	1	HIS5_MYCTU		06589 mycobacteri
10	27	100.0	206	1	HIS5_MYCRU		06043 corynebacte
11	27	100.0	211	1	HIS5_COEGL		P1249 streptomyce
12	27	100.0	222	1	HIS5_STRCO		Q1519 mycobacteri
13	27	100.0	255	1	YM37_MYCTU		P77898 mycobacteri
14	27	100.0	274	1	DCOP_MYCTU		Q05323 mycobacteri
15	27	100.0	276	1	DCOP_MYCSM		Q50658 mycobacteri
16	27	100.0	281	1	YN07_MYCTU		P22495 pseudomonas
17	27	100.0	283	1	PHAB_PSEOL		P97826 rattus norv
18	27	100.0	284	1	STAR_RAT		P34423 bacillus su
19	27	100.0	294	1	YQXK_BACSU		P12114 caenorhabdi
20	27	100.0	324	1	CCSI_CAEEL		P77777 mycobacteri
21	27	100.0	334	1	YE96_MYCTU		Q33980 serratio ma
22	27	100.0	374	1	OMPf_SERMA		Q16699 mycobacteri
23	27	100.0	393	1	EX53_MYCTU		P32426 streptomyce
24	27	100.0	402	1	YIN2_STROM		P56194 thermus aqu
25	27	100.0	421	1	SYH_THETH		P42416 arabiopsis
26	27	100.0	478	1	GSHB_ARATH		Q55714 pseudomonas
27	27	100.0	479	1	CATA_PSEU		Q27710 caenorhabdi
28	27	100.0	482	1	CATA_ONCPE		P96727 caenorhabdi
29	27	100.0	488	1	U2AE_CAEEL		P99778 caenorhabdi
30	27	100.0	496	1	CP46_RABTT		CP4581 oryctolagus
31	27	100.0	510	1	CP47_RABTT		P306581 oryctolagus
32	27	100.0	511	1	CBX2_MOUSE		P306582 mus musculu
33	27	100.0	519	1			Caenorhabditis elegans

ALIGNMENTS

RESULT 1	YMU3_STROM	STANDARD;	PRT;	93 AA.
ID	YMU3_STROM			
AC	005072;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
*	DT 15-DEC-1998 (Rel. 37, Last annotation update)			
DE	HYPOTHETICAL PROTEIN IN MUTB 3' REGION (ORF-C) (FRAGMENT).			
OS	Streptomyces cinnamoneus.			
OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Streptomyces cinnamoneus; Streptomyctaceae; Streptomyces.			
NCBI_TAXID	1900;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=A3823; 5;			
RX	MEDLINE=33273120; PubMed=8099072;			
RA	Birch A., Leiser A., Robinson J.A.;			
RT	"Cloning, sequencing, and expression of the gene encoding methylmalonyl coenzyme A mutase from Streptomyces cinnamoneus."			
RL	J. Bacteriol. 175:3511-3519(1993).			
-1	- SIMILARITY: BELONGS TO THE ARGK FAMILY.			
CC	CC			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	CC			
DR	EMBL; Li0064; AAA03042; 1; -.			
DR	PIR; C40595; C40595;			
KW	Hypothetical protein.			
FT	NON_TER 93			
SEQUENCE	93 AA; 9858 MW; E667DD645B3845D3 CRC64;			
Query	Match	Similarity	Score	Length
Best Local Matches	5	Conservative	100.0%; 100.0%	27; 1;
Mismatches	5	0;	Pred. No. 51;	51;
Indels	0;		Mismatches	0;
Gaps	0;		Indels	0;

SUMMARIES

SUMMARY

Result No.	Score	Query	Match	Length	DB	ID	Description
1	27	100.0	93	1	YMU3_STROM		Q5072 streptomyce
2	27	100.0	128	1	COXE_CAEEL		Q20779 caenorhabdi
3	27	100.0	181	1	Y65L_HORVU		Q4609 hordeum vul
4	27	100.0	192	1	KADA_METTA		P42408 methanococc
5	27	100.0	192	1	KADA_METTL		P42409 methanococc
6	27	100.0	192	1	KADA_METTO		P42410 methanococc
7	27	100.0	192	1	KADA_AERPE		P93d2 aeroprum P
8	27	100.0	204	1	HIS5_MYCIE		Q957c0 mycobacteri
9	27	100.0	206	1	HIS5_MYCTU		06589 mycobacteri
10	27	100.0	206	1	HIS5_MYCRU		06043 corynebacte
11	27	100.0	211	1	HIS5_COEGL		P1249 streptomyce
12	27	100.0	222	1	HIS5_STRCO		Q1519 mycobacteri
13	27	100.0	255	1	YM37_MYCTU		P77898 mycobacteri
14	27	100.0	274	1	DCOP_MYCTU		Q05323 mycobacteri
15	27	100.0	276	1	DCOP_MYCSM		Q50658 mycobacteri
16	27	100.0	281	1	YN07_MYCTU		P22495 pseudomonas
17	27	100.0	283	1	PHAB_PSEOL		P97826 rattus norv
18	27	100.0	284	1	STAR_RAT		P34423 bacillus su
19	27	100.0	294	1	YQXK_BACSU		P12114 caenorhabdi
20	27	100.0	324	1	CCSI_CAEEL		P77777 mycobacteri
21	27	100.0	334	1	YE96_MYCTU		Q33980 serratio ma
22	27	100.0	374	1	OMPf_SERMA		Q16699 mycobacteri
23	27	100.0	393	1	EX53_MYCTU		P32426 streptomyce
24	27	100.0	402	1	YIN2_STROM		P56194 thermus aqu
25	27	100.0	421	1	SYH_THETH		P42416 arabiopsis
26	27	100.0	478	1	GSHB_ARATH		Q55714 pseudomonas
27	27	100.0	479	1	CATA_PSEU		Q27710 caenorhabdi
28	27	100.0	482	1	CATA_ONCPE		P96727 caenorhabdi
29	27	100.0	488	1	U2AE_CAEEL		P99778 caenorhabdi
30	27	100.0	496	1	CP46_RABTT		CP4581 oryctolagus
31	27	100.0	510	1	CP47_RABTT		P306581 oryctolagus
32	27	100.0	511	1	CBX2_MOUSE		P306582 mus musculu
33	27	100.0	519	1			Caenorhabditis elegans

SUMMARY

RESULT 2	COE_CAEEL	STANDARD;	PRT;	128 AA.
ID	COE_CAEEL			
AC	Q20779;			
DT	01-NOV-1997 (Rel. 35, Created)			
QY	1 VPGVG 5			
Db	41 VPGVG 45			
Query	Match	Similarity	Score	Length
Best Local Matches	5	Conservative	100.0%; 100.0%	27; 1;
Mismatches	5	0;	Mismatches	0;
Indels	0;		Indels	0;
Gaps	0;		Gaps	0;

Best Local Similarity 100.0%; Pred. No. lef+02; Mismatches 0; Indels 0; Gaps 0;

Qy	1 VPGVG 5	
Db	11 VPSVG 15	

RESULT 5

KADA_METJA	STANDARD;	PRT;	192 AA.
AC P43409;			
DT 01-NOV-1995 (Rel. 32, Created)			
DT 01-OCT-1996 (Rel. 34, Last sequence update)			
DT 01-OCT-2000 (Rel. 40, Last annotation update)			
ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE).			
GN ADEKA OR ADK OR M00479.			
OS Methanococcus jannaschii.			
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;			
OC Methanococcus.			
OX NCBI_TAXID=2190;			
RN SEQUENCE FROM N.A.			
RX MEDLINE=97208879; PubMed=9055821;			
RA Ferber D.M., Haney P.J., Berk H., Lynn D., Konisky J.;			
RT "The adenylylate kinase genes of <i>M. voltae</i> , <i>M. thermolithotrophicus</i> , <i>M. jannaschii</i> , and <i>M. igneus</i> define a new family of adenylylate kinases.";			
RL Gene 185:239-244 (1997).			
RN [2]			
RP SEQUENCE FROM N.A.			
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;			
RX MEDLINE=96331999; PubMed=8688087;			
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.J., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock G.K., Merrick J.M., Glodek A., Scott J.L., Geoghegan N.S.M., Waldman J.F., Funckmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;			
RT "Complete genome sequence of the methanogenic archaeon, <i>Methanococcus jannaschii</i> ".			
RN Science 273:1058-1073(1996).			
RN [3]			
RP SEQUENCE OF 1-30.			
RX MEDLINE=95288473; PubMed=7768791;			
RA Rusnak P., Haney P., Konisky J.;			
RT "The adenylylate kinases from a mesophilic and three thermophilic methanogenic members of the Archaea.";			
RL J. Bacteriol. 177:2977-2981 (1995).			
CC -1 CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.			
CC -1 SUBUNIT: MONOMER (PROBABLE).			
CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC -1 MISCELLANEOUS: ACTIVE IN THE TEMPERATURE RANGE OF 60 TO 80 DEGREES CELSIUS.			
CC -1 SIMILARITY: BELONGS TO THE ARCHAEL ADENYLATE KINASE FAMILY.			
RN [4]			
RP SEQUENCE OF 1-30.			
RX MEDLINE=95288473; PubMed=7768791;			
RA Rusnak P., Haney P., Konisky J.;			
RT "The adenylylate kinases from a mesophilic and three thermophilic methanogenic members of the Archaea.";			
RL J. Bacteriol. 177:2977-2981 (1995).			
CC -1 CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.			
CC -1 SUBUNIT: MONOMER (PROBABLE).			
CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC -1 MISCELLANEOUS: ACTIVE IN THE TEMPERATURE RANGE OF 70 TO 90 DEGREES CELSIUS.			
CC -1 SIMILARITY: BELONGS TO THE ARCHAEL ADENYLATE KINASE FAMILY.			
RN [5]			
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CC DR U39880; AAC44864.1;			
CC KW Transferase; Kinase; ATP-binding.			
CC FT NP_BIND 10 18 ATP (BY SIMILARITY).			
CC FT CONFLICT 16 16 S -> G (IN REF. 3).			
CC SEQUENCE 192 AA; 21772 MW; EC0533AD4C85D99E CRC64;			
CC SQ Query Match 100.0%; Score 27; DB 1; Length 192;			
CC DR U39882; AAC44863.1;			
CC DR EMBL; U67498; ARB; ARB8470.1; ALT_INIT.			
CC DR TIGR; M00479;			
CC KW Transf erase; Kinase; ATP-binding.			
CC FT NP_BIND 10 18 ATP (BY SIMILARITY).			
CC FT CONFLICT 16 16 S -> G (IN REF. 3).			
CC SEQUENCE 192 AA; 21772 MW; EC0533AD4C85D99E CRC64;			

RESULT 6

KADA_METTL	STANDARD;	PRT;	192 AA.
ID KADA_METTL			
AC P43410;			
DT 01-NOV-1995 (Rel. 32, Created)			
DT 01-OCT-1996 (Rel. 34, Last sequence update)			
DT 01-OCT-2000 (Rel. 40, Last annotation update)			
DE ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE).			
GN ADA OR ADK.			
OS Methanococcus thermolithotrophicus.			
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;			
OC Methanococcus.			
OX NCBI_TAXID=2186;			
OX NCBL_TAXID=2186;			

RESULT 7

KADA_METVO	STANDARD;	PRT;	192 AA.
ID KADA_METVO			
AC P43411;			
DT 01-NOV-1995 (Rel. 32, Created)			
DT 01-OCT-1996 (Rel. 34, Last sequence update)			
DT 01-OCT-2000 (Rel. 40, Last annotation update)			
DE ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE).			

SQ	SEQUENCE	206 AA;	21652 MW;	72D6994084F81536 CRC64;			Db	47 VPGVG 51
	Query Match	100.0%	Score 27;	DB 1;	Length 206;			
	Best Local Similarity	100.0%	Pred. No. 1.1e+02;					
	Matches 5;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;			
QY	1 VPGVG 5							
DB	47 VPGVG 51							
RESULT 10								
HS55_MYCTU	ID HS55_MYCTU	STANDARD;	PRT;	206 AA.				
AC 006589;	AC							
DT 01-OCT-2000 (Rel. 40, Created)	DT							
DT 01-OCT-2000 (Rel. 40, Last sequence update)	DT							
DT 01-OCT-2000 (Rel. 40, Last annotation update)	DT							
DIE AMIDOTRANSFERASE HISH (EC 2.4.2.-).	DIE							
GN HISH OR RV1602 OR MTCT336_03C.	GN							
OS Mycobacterium tuberculosis.	OS							
Bacteria; Firmicutes; Actinobacteria; Actinomycetaceae;	Bacteria;							
Actinomycetales; Corynebacterineae; Mycobacteriaceae;	Actinomycetales;							
NCBI_TAXID=1773; [1]	NCBI_TAXID=1773;							
RP SEQUENCE FROM N.A.	RP							
RC STRAIN=H37RV;	RC							
RX MEDLINE=98295987; PubMed=9634230;	RX							
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,	RA							
RA Gordon S.V., Eiglemeier K., Gas S., Barry C.E. III, Tekala F.,	RA							
RA Bedcock K., Basham D., Brown D., Chillingworth T., Connor R.,	RA							
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Hollroyd S.,	RA							
RA Hornsby T., Jagels K., Krogh A., McLean J., Mole S., Murphy L.,	RA							
RA Oliver S., Quail M.A., Rajandream M.A., Rogers J.,	RA							
RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,	RA							
RA Taylor K., Whitehead S., Barrell B.G.;	RA							
RT Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";	RT							
RT Nature 393:337-354 (1998).	RT							
CC -I- FUNCTION: CATALYZES AN AMIDOTRANSFERASE REACTION THAT GENERATES IMIDAZOLE-GLYCEROL PHOSPHATE AND 5-AMINOIMIDAZOL-4-CARBOXAMIDE RIBONUCLEOTIDE, WHICH IS USED FOR PURINE SYNTHESIS.	CC							
CC -I- PATHWAY: FIFTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.	CC							
CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).	CC							
CC -I- SIMILARITY: BELONGS TO THE HISH FAMILY.	CC							
CC -I- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.	CC							
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DR EMBL: 295586; CAB09092.1; -.	DR							
DR Tuberculist: Rv1602; -.	DR							
DR InterPro; IPR000991; -.	DR							
DR Pfam; PF00117; GATase; 1.	DR							
DR PROSITE; PS00442; GATASE_TYPE_I; 1.	DR							
KW Histidine biosynthesis; Transferase; Glutamine amidotransferase.	KW							
ACT SITE 83 BY SIMILARITY.	ACT SITE	83	BY SIMILARITY.					
FT ACT SITE 187 BY SIMILARITY.	FT	187	BY SIMILARITY.					
FT ACT SITE 189 BY SIMILARITY.	FT	189	BY SIMILARITY.					
SQ SEQUENCE 206 AA; 21418 MW; 4B2AFF961BEB1447 CRC64;	SQ	206 AA;	21418 MW;	4B2AFF961BEB1447 CRC64;				
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC							
DR EMBL: 295586; CAB09092.1; -.	DR							
DR InterPro; IPR000991; -.	DR							
DR Pfam; PF00117; GATase; 1.	DR							
DR PROSITE; PS00442; GATASE_TYPE_I; 1.	DR							
KW Histidine biosynthesis; Transferase; Glutamine amidotransferase.	KW							
ACT SITE 83 BY SIMILARITY.	ACT SITE	83	BY SIMILARITY.					
FT ACT SITE 187 BY SIMILARITY.	FT	187	BY SIMILARITY.					
FT ACT SITE 189 BY SIMILARITY.	FT	189	BY SIMILARITY.					
SQ SEQUENCE 206 AA; 21418 MW; 4B2AFF961BEB1447 CRC64;	SQ	206 AA;	21418 MW;	4B2AFF961BEB1447 CRC64;				
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DR EMBL: 295586; CAB09092.1; -.	DR							
DR InterPro; IPR000991; -.	DR							
DR Pfam; PF00117; GATase; 1.	DR							
DR PROSITE; PS00442; GATASE_TYPE_I; 1.	DR							
KW Histidine biosynthesis; Transferase; Glutamine amidotransferase.	KW							
ACT SITE 83 BY SIMILARITY.	ACT SITE	83	BY SIMILARITY.					
FT ACT SITE 187 BY SIMILARITY.	FT	187	BY SIMILARITY.					
FT ACT SITE 189 BY SIMILARITY.	FT	189	BY SIMILARITY.					
SQ SEQUENCE 206 AA; 21418 MW; 4B2AFF961BEB1447 CRC64;	SQ	206 AA;	21418 MW;	4B2AFF961BEB1447 CRC64;				
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC							
DR EMBL: 295586; CAB09092.1; -.	DR							
DR InterPro; IPR000991; -.	DR							
DR Pfam; PF00117; GATase; 1.	DR							
DR PROSITE; PS00442; GATASE_TYPE_I; 1.	DR							
KW Histidine biosynthesis; Transferase; Glutamine amidotransferase.	KW							
ACT SITE 83 BY SIMILARITY.	ACT SITE	83	BY SIMILARITY.					
FT ACT SITE 187 BY SIMILARITY.	FT	187	BY SIMILARITY.					
FT ACT SITE 189 BY SIMILARITY.	FT	189	BY SIMILARITY.					
SQ SEQUENCE 206 AA; 21418 MW; 4B2AFF961BEB1447 CRC64;	SQ	206 AA;	21418 MW;	4B2AFF961BEB1447 CRC64;				
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DR EMBL: 295586; CAB09092.1; -.	DR							
DR InterPro; IPR000991; -.	DR							
DR Pfam; PF00117; GATase; 1.	DR							
DR PROSITE; PS00442; GATASE_TYPE_I; 1.	DR							
KW Histidine biosynthesis; Transferase; Glutamine amidotransferase.	KW							
ACT SITE 83 BY SIMILARITY.	ACT SITE	83	BY SIMILARITY.					
FT ACT SITE 187 BY SIMILARITY.	FT	187	BY SIMILARITY.					
FT ACT SITE 189 BY SIMILARITY.	FT	189	BY SIMILARITY.					
SQ SEQUENCE 206 AA; 21418 MW; 4B2AFF961BEB1447 CRC64;	SQ	206 AA;	21418 MW;	4B2AFF961BEB1447 CRC64;				
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DR EMBL: 295586; CAB09092.1; -.	DR							
DR InterPro; IPR000991; -.	DR							
DR Pfam; PF00117; GATase; 1.	DR							
DR PROSITE; PS00442; GATASE_TYPE_I; 1.	DR							
KW Histidine biosynthesis; Transferase; Glutamine amidotransferase.	KW							
ACT SITE 83 BY SIMILARITY.	ACT SITE	83	BY SIMILARITY.					
FT ACT SITE 187 BY SIMILARITY.	FT	187	BY SIMILARITY.					
FT ACT SITE 189 BY SIMILARITY.	FT	189	BY SIMILARITY.					
SQ SEQUENCE 206 AA; 21418 MW; 4B2AFF961BEB1447 CRC64;	SQ	206 AA;	21418 MW;	4B2AFF961BEB1447 CRC64;				
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DR EMBL: 295586; CAB09092.1; -.	DR							
DR InterPro; IPR000991; -.	DR							
DR Pfam; PF00117; GATase; 1.	DR							
DR PROSITE; PS00442; GATASE_TYPE_I; 1.	DR							
KW Histidine biosynthesis; Transferase; Glutamine amidotransferase.	KW							
ACT SITE 83 BY SIMILARITY.	ACT SITE	83	BY SIMILARITY.					
FT ACT SITE 187 BY SIMILARITY.	FT	187	BY SIMILARITY.					
FT ACT SITE 189 BY SIMILARITY.	FT	189	BY SIMILARITY.					
SQ SEQUENCE 206 AA; 21418 MW; 4B2AFF961BEB1447 CRC64;	SQ	206 AA;	21418 MW;	4B2AFF961BEB1447 CRC64;				
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DR EMBL: 295586; CAB09092.1; -.	DR							
DR InterPro; IPR000991; -.	DR							
DR Pfam; PF00117; GATase; 1.	DR							
DR PROSITE; PS00442; GATASE_TYPE_I; 1.	DR							
KW Histidine biosynthesis; Transferase; Glutamine amidotransferase.	KW							
ACT SITE 83 BY SIMILARITY.	ACT SITE	83	BY SIMILARITY.					
FT ACT SITE 187 BY SIMILARITY.	FT	187	BY SIMILARITY.					
FT ACT SITE 189 BY SIMILARITY.	FT	189	BY SIMILARITY.					
SQ SEQUENCE 206 AA; 21418 MW; 4B2AFF961BEB1447 CRC64;	SQ	206 AA;	21418 MW;	4B2AFF961BEB1447 CRC64;				
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DR EMBL: 295586; CAB09092.1; -.	DR							
DR InterPro; IPR000991; -.	DR							
DR Pfam; PF00117; GATase; 1.	DR							
DR PROSITE; PS00442; GATASE_TYPE_I; 1.	DR							
KW Histidine biosynthesis; Transferase; Glutamine amidotransferase.	KW							
ACT SITE 83 BY SIMILARITY.	ACT SITE	83	BY SIMILARITY.					
FT ACT SITE 187 BY SIMILARITY.	FT	187	BY SIMILARITY.					
FT ACT SITE 189 BY SIMILARITY.	FT	189	BY SIMILARITY.					
SQ SEQUENCE 206 AA; 21418 MW; 4B2AFF961BEB1447 CRC64;	SQ	206 AA;	21418 MW;	4B2AFF961BEB1447 CRC64;				
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DR EMBL: 295586; CAB09092.1; -.	DR							
DR InterPro; IPR000991; -.	DR							
DR Pfam; PF00117; GATase; 1.	DR							
DR PROSITE; PS00442; GATASE_TYPE_I; 1.	DR							
KW Histidine biosynthesis; Transferase; Glutamine amidotransferase.	KW							
ACT SITE 83 BY SIMILARITY.	ACT SITE	83	BY SIMILARITY.					
FT ACT SITE 187 BY SIMILARITY.	FT	187	BY SIMILARITY.					
FT ACT SITE 189 BY SIMILARITY.	FT	189	BY SIMILARITY.					
SQ SEQUENCE 206 AA; 21418 MW; 4B2AFF961BEB1447 CRC64;	SQ	206 AA;	21418 MW;	4B2AFF961BEB1447 CRC64;				
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DR EMBL: 295586; CAB09092.1; -.	DR							
DR InterPro; IPR000991; -.	DR							
DR Pfam; PF00117; GATase; 1.	DR							
DR PROSITE; PS00442; GATASE_TYPE_I; 1.	DR							
KW Histidine biosynthesis; Transferase; Glutamine amidotransferase.	KW							
ACT SITE 83 BY SIMILARITY.	ACT SITE	83	BY SIMILARITY.					
FT ACT SITE 187 BY SIMILARITY.	FT	187	BY SIMILARITY.					
FT ACT SITE 189 BY SIMILARITY.	FT	189	BY SIMILARITY.					
SQ SEQUENCE 206 AA; 21418 MW; 4B2AFF961BEB1447 CRC64;	SQ	206 AA;	21418 MW;	4B2AFF961BEB1447 CRC64;				
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DR EMBL: 295586; CAB09092.1; -.	DR							

SEQUENCE FROM N.A.

RP STRAIN=A3(2);
RX MEDLINE=90337345; PubMed=2199329;

RA Limauro D., Avitabile A., Cappellano M., Puglia A.M., Bruni C.B.;
RT Cloning and characterization of the histidine biosynthetic gene
cluster of Streptomyces coelicolor A3(2)." ;
RN Gene 90:31-41(1990).

[2]

SEQUENCE FROM N.A.

RP STRAIN=A3(2);
RA Seeger K., Harris D., Bentley S.D., Parkhill J., Barrell B.G.,
RA Rajandream M.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: CATALYZES AN AMIDOTRANSFERASE REACTION THAT GENERATES
IMIDAZOLE-GLYCEROL PHOSPHATE AND 5-AMINOMIDAZOL-4-CARBOXYAMIDE
RIBONUCLEOTIDE, WHICH IS USED FOR PURINE SYNTHESIS.
CC -I- PATHWAY: FIFTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.
CC -I- SUBCELLULAR LOCATION: CYTOPLASMATIC (PROBABLE).
CC -I- SIMILARITY: BELONGS TO THE HISF FAMILY.
CC -I- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.

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CC DR EMBL: M31628; AAA26759; 1; -;
DR EMBL: AL096884; CAB51443; 1; -;
DR InterPro: IPR000991; -;
DR Pfam: PF00117; GATase; 1;
DR PROSITE: PS0042; GATASE_TYPE_I; 1;
KW Histidine biosynthesis; Transferase; Glutamine amidotransferase.

FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 203 203 BY SIMILARITY.
FT ACT_SITE 205 205 BY SIMILARITY.

SEQUENCE 222 AA; 23861 MW; C075CB4354744CB6 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPGVG 5
Db 57 VPGVG 61

RESULT 13
YMA37_MYCTU STANDARD; PRT; 255 AA.

AC Q10519;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE HYPOTHETICAL PROTEIN RV2237.
DN RV2237 OR MTCY427 18.

OS Mycobacterium tuberculosis.

OC Bacteria; Firmicutes; Actinobacteria; Corynebacteriaceae; Mycobacterium.

OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacteriaceae; Mycobacterium.

OX NCBL_TAXID=1773;

RN SEQUENCE FROM N.A.

RP STRAIN=H37RV;
RC MEDLINE=9825987; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglemeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Shelton S., Whitehead S., Barrell B.G.,
RA Taylor K., Whitehead S., Barrell B.G.,
RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence." ;
RL Nature 393:537-544(1998).

[2]

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CC DR EMBL: Z70632; CRA94667; 1; -;
DR TubercuList; RV2237; -;
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 2 22 POTENTIAL.
FT TRANSMEM 168 188 POTENTIAL.

SEQUENCE 255 AA; 29067 MW; B0F42277C6B46A6 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPGVG 5
Db 14 VPGVG 18

RESULT 14
DCOP_MYCTU STANDARD; PRT; 274 AA.

ID DCOP_MYCTU ID P77838; P42610;
AC DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE OROTIDINE 5'-PHOSPHATE DECARBOXYLASE (EC 4.1.1.23) (OMP
DECARBOXYLASE) (OMPDCASE).

GN PYRF OR URAA OR RV1385 OR MTCY21B1-02.

OS Mycobacterium tuberculosis, and Mycobacterium bovis.

OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacteriaceae; Mycobacterium.

OX NCBL_TAXID=1773; 1765;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=H37RV;

RX MEDLINE=28295387; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglemeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Shelton S., Whitehead S., Barrell B.G.,
RA Taylor K., Whitehead S., Barrell B.G.,
RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence." ;
RL Nature 393:537-544(1998).

[2]

CC SEQUENCE FROM N.A.

RC SPECIES=M.bovis; STRAIN=BCG;

RX MEDLINE=14012902; PubMed=8226675;

RA Aldovini A., Husson R.N., Young R.A.;
RT "The uraA locus and homologous recombination in Mycobacterium bovis BCG";
RL J. Bacteriol. 175:7282-7289(1993).

CC -I- CATALYTIC ACTIVITY: OROTIDINE 5'-PHOSPHATE + CO(2).

CC -I- PATHWAY: SIXTH AND LAST STEP IN THE BIOSYNTHESIS OF PRIMIDINES.

CC -I- SIMILARITY: BELONGS TO THE OMP DECARBOXYLASE FAMILY.

CC

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```
DR EMBL; 280108; CAB02190 1;
DR U01072; AAC3182.1; -
DR Tuberculist; Rv1385; -
DR InterPro; IPR001554; -
DR Pfam; PF00215; OMPdecase; 1;
DR PROSITE; PS00156; OMPDCASE; 1;
DR Pyrimidine biosynthesis; Lyase; Decarboxylase.
FT ACT_SITE 95 95 BY SIMILARITY.
SQ SEQUENCE 274 AA; 27377 MW; 369BAR076FB3D143 CRC64;
```

Query Match 100.0%; Score 27; DB 1; Length 274;

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;

Qy	1 VPGVG 5
Db	215 VPGVG 219

```
RESULT 15
DCOP_MYCSM STANDARD PRT; 276 AA.
ID DCOP_MYCSM STANDARD; PRT; 276 AA.
AC 008323;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OROTIDINE 5'-PHOSPHATE DECARBOXYLASE (EC 4.1.1.23) (OMP
DECARBOXYLASE) (OMPDCASE).
GN PYRF.
OS Mycobacterium smegmatis.
OC Bacteria: Firmicutes: Actinobacteria: Actinomycetidae;
AC Actinomycetales: Corynebacterineae; Mycobacterium.
OC NCBI_TAXID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAINATCC 700084 / MC(2)155;
RX MEDLINE=97312763; Published=9169204;
RA Knipef, N., Seth A., Shrader T.E. ;
RR "Unmarked gene integration into the chromosome of Mycobacterium
smegmatis via precise replacement of the PYRF gene." ;
RL Plasmid 37:129-140 (1997).
CC -1- CATALYTIC ACTIVITY: OROTIDINE 5'-PHOSPHATE = UMP + CO(2).
CC -1- PATHWAY: SIXTH AND LAST STEP IN THE BIOSYNTHESIS OF PYRIMIDINES.
CC -1- SUBUNIT: OMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE OMP DECARBOXYLASE FAMILY.
```

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```
DR EMBL; U91572; AAB0157.1;
DR InterPro; IPR001554; -
DR Pfam; PF00215; OMPdecase; 1;
DR PROSITE; PS00156; OMPDCASE; 1;
DR Pyrimidine biosynthesis; Lyase; Decarboxylase.
FT ACT_SITE 95 95 BY SIMILARITY.
SQ SEQUENCE 276 AA; 27815 MW; 41437043A3E2A896 CRC64;
```

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
 |||

Db 221 VPGVG 225

Search completed: July 25, 2001, 16:51:25
Job time: 156 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 25, 2001, 16:48:49 ; Search time 33.32 Seconds

(without alignments)
19.854 Million cell updates/secTitle: US-09-251-638-1
Perfect score: 27
Sequence: 1 vpsvg 5Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :	SPTREMBL_16:*
1:	sp_archaea:*
2:	sp_bacteria:*
3:	sp_fungi:*
4:	sp_human:*
5:	sp_invertebrate:*
6:	sp_mammal:*
7:	sp_mhc:*
8:	sp_organelle:*
9:	sp_phage:*
10:	sp_plant:*
11:	sp_rrodent:*
12:	sp_unclassified:*
13:	sp_vertebrate:*
14:	sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	27	100.0	38	2	005422		005422 mycobacteri
2	27	100.0	76	6	028100		Q28100 bos taurus
3	27	100.0	100	4	09H402		Q9H402 homo sapien
4	27	100.0	120	2	09RJ6		Q9RJ6 deinococcus
5	27	100.0	127	2	Q9YD00		Q9YD00 aeropyrum p
6	27	100.0	130	6	018832		Q18832 equus caballus
7	27	100.0	138	1	09HHZ4		Q9HHZ4 halobacteri
8	27	100.0	139	2	P71912		P71912 mycobacteri
9	27	100.0	141	2	066301		066301 unidentified
10	27	100.0	141	2	066330		066330 unidentified
11	27	100.0	141	2	066336		066336 unidentified
12	27	100.0	141	2	066364		066364 unidentified
13	27	100.0	141	2	066365		066365 unidentified
14	27	100.0	141	2	066367		066367 unidentified
15	27	100.0	143	5	Q9NZX5		Q9NZX5 caenorhabditis
16	27	100.0	162	10	Q9TIR0		Q9TIR0 arabidopsis
17	27	100.0	167	5	Q9V506		Q9V506 drosophila
18	27	100.0	169	13	Q9PVQ0		Q9PVQ0 xenopus laevis
19	27	100.0	170	2	Q9KGF1		Q9KGF1 bacillus haemolyticus

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	PRT;
ID	005422			
AC	005422;			
DT	01-JUL-1997 (TREMBLrel. 04, Created)			
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)			
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)			
DE	PHYOENE DEHYDROGENASE (FRAGMENT).			
GN	CRTI			
OS	Mycobacterium marinum.			
OC	Bacteria; Firmicutes; Actinomycetales; Corynebacteriaceae; Mycobacterium.			
OX	NCBI_TaxID=1781;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=M;			
RX	MEDLINE=97440138; PubMed=9294446;			
RA	Ramakrishnan L., Tran H.T., Federpiel N.A., Falkow S.; "A crtB homolog essential for photochromogenicity in Mycobacterium marinum: isolation, characterization, and gene disruption via homologous recombination."			
RT	J. Bacteriol. 179:5862-5868 (1997).			
RL	EMBL; U92075; AAB71427.1; -			
DR	NON_TER	1	1	
SQ	SEQUENCE	38 AA;	3986 MW;	6E45332707CCDCAB CRC64;

Query Match 100.0%; Score 27; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 91; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5

Db 1 VPGVG 5

RESULT 2

Q28100 PRELIMINARY; PRT; 76 AA.

AC Q9V506

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)	RN [1]
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)	RP SEQUENCE FROM N.A.
DE	(CSPCP) (FRAGMENT).	RX MEDLINE=20504483; PubMed=11016950;
GN	AGC1.	RA NG W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M., Shukla H.D., Lasky S.R., Thorsson V., Sbrrogna J., Swarzelli S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danzon M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlischroder M., Spudich J.L., Jung K., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebbhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; RT "Genome sequence of Halobacterium species NRC-1." RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000); DR EMBL; AE005152; ARG20828.1; -.
OS	Equus caballus (horse); Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.	RX
OC	[1]	RN
OX	RP SEQUENCE FROM N.A.	RX
RT	TISSUE=C-H8209637; PubMed=9550267;	RX
RA	Flannery C.R., Little C.B., Caterson B.;	RX
RR	"Molecular cloning and sequence analysis of the aggrecan interglobular domain from porcine, equine, bovine and ovine cartilage: comparison of protease-susceptible regions and sites of keratan sulfate substitution.";	RX
RL	Matrix Biol. 16:507-511(1997).	RX
CC	-1- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CARTILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION. MAY PLAY A REGULATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.	RX
CC	-1- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR MATRIX (By SIMILARITY).	RX
CC	-1- DOMAIN: TWO GLOBULAR DOMAINS, G1 AND G2, COMprise THE AMINO TERMINUS OF THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS. G1 CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, B MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS) AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS lie BETWEEN G2 AND G3.	RX
CC	-1- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE CHAINS, N-LINKED AND O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).	RX
CC	-1- SIMILARITY: BELONGS TO THE AGGREGAN/VERSICAN PROTEOGLYCAN FAMILY.	RX
DR	EMBL; AF019756; AAC48198.1; -.	RX
DR	InterPro; IPR000538; -.	RX
DR	PROSITE; PS01241; LINK; PARTIAL.	RX
KW	GLycoprotein; Cartilage; Proteoglycan; Repeat.	RX
FT	NON_TER 1 1	RN
FT	NON_TER 1 1	RP SEQUENCE FROM N.A.
FT	LINK 2.	RC STRAIN=H37RV;
FT	G1-'.	RX MEDLINE=98295087; PubMed=9634230;
FT	10	RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E., III, Tekwaria F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feitwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rogers J., Rutter S., Seeger K., Shelton S., Squares S., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; RL Nature 393:537-544(1998); DR EMBL; 281451; CAB03782.1; -.
FT	48	KW Hypothetical protein.
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).	SQ SEQUENCE 139 AA; 13830 MW; 082F79B5AE78B53E CRC64;
FT	95	RN 139 AA; 15315 MW; 842BF116C0E102EC CRC64;
FT	130	Query Match Score 27; DB 6; Length 130; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Mismatches 0; Indels 0; Gaps 0;
FT	130	Query Match Score 27; DB 2; Length 139; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Mismatches 0; Indels 0; Gaps 0;
SQ	130 AA; 13830 MW; 082F79B5AE78B53E CRC64;	QY 1 VPGVG 5
RESULT	7	DB 82 VPGVG 86
OSHHZ4	PRELIMINARY;	PRT; 138 AA.
ID	09HHZ4	Query Match Score 27; DB 2; Length 139; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Mismatches 0; Indels 0; Gaps 0;
AC	Q9HHZ4	QY 1 VPGVG 5
DT	01-MAR-2001 (TREMBLrel. 16, Created)	DB 132 VPGVG 136
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	RESULT 9
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	ID 066301 PRELIMINARY; PRT; 141 AA.
DF	VNG6157H.	NCBI_TAXID=64091;
OS	Halobacterium sp. (strain NRC-1).	OS Plasmid pNRC200.
OC	Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;	OC Halobacterium.
OC	Halobacterium.	NCBI_TAXID=64091;

AC 066301; PRELIMINARY; PRT; 141 AA.
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ALPHA SUBUNIT OF DINITROGENASE REDUCTASE (FE PROTEIN) (FRAGMENT).
 GN NIFH.
 OS unidentified nitrogen-fixing bacteria.
 OC Bacteria.
 OX NCBI_TAXID=34107;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohkuma M., Noda S., Kudo T.; EMBL/GenBank/DDJB databases.
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDJB databases.
 DR EMBL; AB01155; BAA28392.1; -.
 HSSP; P00456; ICP2.
 DR InterPro; IPR000392; -.
 DR Pfam; PF00142; fer4_NIFH; 1.
 DR PRINTS; PR00094; NITROGENASEII.
 DR PROSITE; PS00746; NIFH_FRXC_1; 1.
 DR PROSITE; PS00692; NIFH_FRXC_2; 1.
 FT NON-TER 1 141 141 MW; 02454EC055EDBE40 CRC64;
 SQ SEQUENCE 141 AA; 14882 MW; D2E06148699D28C3 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02; Length 141;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
 |||||
 Db 74 VPGVG 78

RESULT 10
 066330 PRELIMINARY; PRT; 141 AA.
 ID 066330
 AC 066330; PRELIMINARY; PRT; 141 AA.
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DE ALPHA SUBUNIT OF DINITROGENASE REDUCTASE (FE PROTEIN) (FRAGMENT).
 GN NIFH.
 OS unidentified nitrogen-fixing bacteria.
 OC Bacteria.
 OX NCBI_TAXID=34107;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohkuma M., Noda S., Kudo T.; EMBL/GenBank/DDJB databases.
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDJB databases.
 DR EMBL; AB01190; BAA28351.1; -.
 HSSP; P00456; ICP2.
 DR InterPro; IPR000392; -.
 DR Pfam; PF00142; fer4_NIFH; 1.
 DR PRINTS; PR00094; NITROGENASEII.
 DR PROSITE; PS00746; NIFH_FRXC_1; 1.
 DR PROSITE; PS00692; NIFH_FRXC_2; 1.
 FT NON-TER 1 141 141 MW; 7251716CF85C6752 CRC64;
 SQ SEQUENCE 141 AA; 14780 MW; E069FA235F62484B CRC64;

Query Match 100.0%; Score 27; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02; Length 141;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
 |||||
 Db 74 VPGVG 78

RESULT 13
 066336
 ID 066336; PRELIMINARY; PRT; 141 AA.
 AC 066336;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ALPHA SUBUNIT OF DINITROGENASE REDUCTASE (FE PROTEIN) (FRAGMENT).
 GN NIFH.
 OS unidentified nitrogen-fixing bacteria.
 OC Bacteria.
 OX NCBI_TAXID=34107;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohkuma M., Noda S., Kudo T.; EMBL/GenBank/DDJB databases.
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDJB databases.
 DR EMBL; AB011906; BAA28441.1; -.
 HSSP; P00456; ICP2.
 DR InterPro; IPR000392; -.
 DR Pfam; PF00142; fer4_NIFH; 1.
 DR PRINTS; PR00091; NITROGENASEII.
 DR PROSITE; PS00746; NIFH_FRXC_1; 1.
 DR PROSITE; PS00692; NIFH_FRXC_2; 1.
 FT NON-TER 1 141 141 MW; D2E06148699D28C3 CRC64;
 SQ SEQUENCE 141 AA; 14910 MW; D2E06148699D28C3 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02; Length 141;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID 066365 PRELIMINARY; PRT; 141 AA.
AC 066365; 1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ALPHA SUBUNIT OF DINITROGENASE REDUCTASE (FE PROTEIN) (FRAGMENT).
GN NIFH
OS unidentified nitrogen-fixing bacteria.
OC Bacteria.
OX NCBI_TaxID=34107;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohkuma M., Noda S., Kudo T.; EMBL/GenBank/DDBJ databases.
RL Submitted (MAR-1995; BAA28488.1; -.
DR EMBL: AB011935; HSSP: P00456; ICP2;
DR InterPro: IPR000399; -.
DR Pfam: PF00142; fer4_NiFH; 1.
DR PROSITE; PS00746; NIFH_FRXC_1; 1.
DR PROSITE; PS00692; NIFH_FRXC_2; 1.
DR NON_TER 1 1
FT NON_TER 141 141
SQ SEQUENCE 141 AA; 14786 MW; 2BC10A2BF5C05E2E CRC64;

Query Match 100.0%; Score 27; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
Db 74 VPGVG 78

RESULT 14
ID 066367 PRELIMINARY; PRT; 141 AA.
AC 066367; 1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ALPHA SUBUNIT OF DINITROGENASE REDUCTASE (FE PROTEIN) (FRAGMENT).
GN NIFH
OS unidentified nitrogen-fixing bacteria.
OC Bacteria.
OX NCBI_TaxID=34107;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohkuma M., Noda S., Kudo T.; EMBL/GenBank/DDBJ databases.
RL Submitted (MAR-1995; BAA284890.1; -.
DR EMBL: AB011937; HSSP: P00456; ICP2;
DR InterPro: IPR000399; -.
DR Pfam: PF00142; fer4_NiFH; 1.
DR PROSITE; PS00746; NIFH_FRXC_1; 1.
DR PROSITE; PS00692; NIFH_FRXC_2; 1.
DR NON_TER 1 1
FT NON_TER 141 141
SQ SEQUENCE 141 AA; 14505 MW; 7A2B008BE564C29C CRC64;

Query Match 100.0%; Score 27; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPGVG 5
Db 74 VPGVG 78

RESULT 15
ID Q9N2X5 PRELIMINARY; PRT; 143 AA.

